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STIC-Biotech/ChemLib

From: Seharaseyon, Jegatheesan
Sent: Monday, June 05, 2006 10:51 AM
To: STIC-Biotech/ChemLib
Subject: Re:10/063540

Please search SEQ ID NO: 34 in the pending and allowed databases.
Also please search with a word size of 6 amino acids.

Thanks

J.Seharaseyon
Art Unit 1647
Remsen 4C61
Mailbox 4C70
Phone: (571)-272-0892
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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

- Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
- Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2006, 01:10:42 ; Search time 302 Seconds
(without alignments)

2076.691 Million cell updates/sec

Title: US-10-063-540-34
Perfect score: 3502
Sequence: 1 MRTVLTMKASVIMFLVL.....QYVPRITQICTFENSPRN 678

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Uniprot_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------------|--------------------|
| 1 | 3502 | 100.0 | 678 | Q6UX17_HUMAN | Q6UX17 homo sapien |
| 2 | 3484.5 | 99.5 | 693 | Q9UDN0_HUMAN | Q9UDN0 homo sapien |
| 3 | 3344 | 95.5 | 656 | Q96DRI_HUMAN | Q96DRI homo sapien |
| 4 | 2826 | 80.7 | 650 | Q3TZ47_MOUSE | Q3TZ47 mus musculu |
| 5 | 2823 | 80.6 | 650 | Q8VH15_MOUSE | Q8VH15 mus musculu |
| 6 | 2818 | 80.5 | 652 | Q95L12_BOVIN | Q95L12 bos taurus |
| 7 | 2801 | 80.0 | 650 | Q8K047_MOUSE | Q8K047 mus musculu |
| 8 | 2796 | 79.8 | 650 | Q9CY21_MOUSE | Q9CY21 mus musculu |
| 9 | 2682 | 76.6 | 628 | Q8B041_MOUSE | Q8B041 mus musculu |
| 10 | 2311.5 | 66.0 | 748 | Q5NTW9_CHICK | Q5NTW9 gallus gall |
| 11 | 1929 | 55.1 | 680 | Q4PZ7_TETNG | Q4PZ7 tetradon n |
| 12 | 1187.5 | 33.9 | 553 | Q8AW56_BRARE | Q8AW56 brachydanto |
| 13 | 1139 | 32.5 | 547 | COCH_CHICK | COCH gallus gall |
| 14 | 1129.5 | 32.3 | 550 | COCH_HUMAN | COCH homo sapien |
| 15 | 1123.5 | 32.1 | 550 | Q5EAF4_BOVIN | Q5EAF4 bos taurus |
| 16 | 1115 | 31.8 | 552 | Q3U021_MOUSE | Q3U021 mus musculu |
| 17 | 1113 | 31.8 | 552 | COCH_MOUSE | COCH mus musculu |
| 18 | 1113 | 31.8 | 552 | Q3TAF5_MOUSE | Q3TAF5 m activat |
| 19 | 1017.5 | 29.1 | 494 | Q96IUG_HUMAN | Q96IUG homo sapien |
| 20 | 1008.5 | 28.8 | 586 | Q4T252_TETNG | Q4T252 tetradon n |
| 21 | 848 | 24.2 | 203 | Q6P7R3_HUMAN | Q6P7R3 homo sapien |
| 22 | 834.5 | 23.8 | 401 | Q6ZP09_HUMAN | Q6ZP09 homo sapien |
| 23 | 554 | 15.8 | 3124 | COCAI_CHICK | COCAI gallus gall |
| 24 | 552 | 15.8 | 3119 | COCAI_MOUSE | COCAI mus musculu |
| 25 | 543.5 | 15.5 | 3063 | COCAI_HUMAN | COCAI homo sapien |
| 26 | 542.5 | 15.5 | 2884 | Q5VYK2_HUMAN | Q5VYK2 homo sapien |
| 27 | 542.5 | 15.5 | 3063 | Q5VYK1_HUMAN | Q5VYK1 homo sapien |
| 28 | 512 | 14.6 | 490 | Q7SYT5_XENLA | Q7SYT5 xenopus lae |
| 29 | 505 | 14.4 | 490 | Q5BKH6_XENTR | Q5BKH6 xenopus tto |
| 30 | 504.5 | 14.4 | 3137 | CO6A3_CHICK | CO6A3 gallus gall |
| 31 | 501.5 | 14.3 | 496 | MATN1_HUMAN | MATN1 homo sapien |

| | | | | | |
|----|-------|------|------|--------------|--------------------|
| 32 | 501.5 | 14.3 | 496 | Q5TB9_HUMAN | Q5TB9 homo sapien |
| 33 | 494.5 | 14.1 | 498 | Q5X124_RAT | Q5X124 ratu |
| 34 | 493 | 14.1 | 500 | Q8OVN5_MOUSE | Q8OVN5 mus musculu |
| 35 | 490 | 14.0 | 493 | MATN1_CHICK | P05099 gallus gall |
| 36 | 490 | 14.0 | 500 | MATN1_MOUSE | P51942 mus musculu |
| 37 | 488.5 | 13.9 | 1259 | Q4RP12_TETNG | Q4RP12 tetradon n |
| 38 | 485 | 13.8 | 507 | Q7ZVP3_BRARE | Q7ZVP3 brachydanto |
| 39 | 478.5 | 13.7 | 644 | Q5NJU1_BRARE | Q5NJU1 brachydanto |
| 40 | 471.5 | 13.5 | 2588 | Q53OF4_HUMAN | Q53OF4 homo sapien |
| 41 | 471.5 | 13.5 | 3176 | CO6A3_HUMAN | P12111 homo sapien |
| 42 | 466 | 13.3 | 3169 | Q4KKT6_CANFA | Q4KKT6 canis famli |
| 43 | 464 | 13.2 | 1453 | Q4RN1_TETNG | Q4RN1 tetradon n |
| 44 | 463 | 13.2 | 1182 | Q8C6K9_MOUSE | Q8C6K9 mus musculu |
| 45 | 459 | 13.1 | 685 | Q5NJU2_BRARE | Q5NJU2 brachydanto |

ALIGNMENTS

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RESULT 1
ID Q6UX17_HUMAN PRELIMINARY; PRT; 678 AA.
AC Q6UX17;
BT 24-MAY-2005, integrated into UniprotKB/TREMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE VIT.
GN ORFNames=UNO647;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagte A.,
RA Vanden R.L., Watanabe C., Weand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
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CC -----
CC EMBL: AY358338; AAC08704.1; -; mRNA.
CC HSSP: Q43405; IUBI.
CC InterPro: IPR004043; LCCL.
CC InterPro: IPR002035; VWF_A.
CC Pfam: PF03815; LCCL; 1.
CC Pfam: PF00092; VWA; 2.
CC PRINTS: PR00453; VWFADOMAIN.
CC SMART: SM00603; LCCL; 1.
CC SMART: SM00327; VWA; 2.
CC PROSITE: PS00820; LCCL; 1.
CC PROSITE: PS50234; VWF_A; 2.
CC SEQUENCE 678 AA; 73530 MW; 9870E75A218C686C CRC64;
Query Match 100.0%; Score 3502; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 3e-219;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MRTVLTMKASVIMFLVLVTGVHSNKEETAKKIKRPFYVPOINCQVKAAGKIIDPEFIV 60
DB 1 MRTVLTMKASVIMFLVLVTGVHSNKEETAKKIKRPFYVPOINCQVKAAGKIIDPEFIV 60

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QY 61 KCPAGCDDPKYHYGTDVYASYSVCGAAVHSGVLDSGGKILVRKYAGOSGYKGSYNG 120
Db 61 KCPAGCDDPKYHYGTDVYASYSVCGAAVHSGVLDSGGKILVRKYAGOSGYKGSYNG 120
QY 121 VQSLSPRMRESFVLESKPKKGYTPSALTYSKSPAAQAGETTAYORPPIPGTTAQ 180
Db 121 VQSLSPRMRESFVLESKPKKGYTPSALTYSKSPAAQAGETTAYORPPIPGTTAQ 180
QY 181 PVTLMQLLAVTAAVATPTTLPRPSPSAASTISIRPQSVGRSQEMDLMSTATTSSQNR 240
Db 181 PVTLMQLLAVTAAVATPTTLPRPSPSAASTISIRPQSVGRSQEMDLMSTATTSSQNR 240
QY 241 PRADPGIORODPSGAAPQKPGAVGVSGLVYKEELSTQSLPEVSLGDPNCKIDSLPILDG 300
Db 241 PRADPGIORODPSGAAPQKPGAVGVSGLVYKEELSTQSLPEVSLGDPNCKIDSLPILDG 300
QY 301 STSIGKRFRIOQLDLADVAQALDIPAGPLMGVVOYGDNDPAPHNLKTHNTSSDLKTAI 360
Db 301 STSIGKRFRIOQLDLADVAQALDIPAGPLMGVVOYGDNDPAPHNLKTHNTSSDLKTAI 360
QY 361 EKTORRGLSNVGAISFTYKNFSSKANGNSGAPNVVVVWDMPDVKVEASRLARES 420
Db 361 EKTORRGLSNVGAISFTYKNFSSKANGNSGAPNVVVVWDMPDVKVEASRLARES 420
QY 421 GINIFFTITGGAENKQYVVEPNPANKAVCRITNGFYSLSHYQSFGLHKTLOPLVKRVC 480
Db 421 GINIFFTITGGAENKQYVVEPNPANKAVCRITNGFYSLSHYQSFGLHKTLOPLVKRVC 480
QY 481 TDLRACSKTCLNSADIGFVIDSSSVGTGNFRVLAQVNTLTKPEISDTRIGAVOYT 540
Db 481 TDLRACSKTCLNSADIGFVIDSSSVGTGNFRVLAQVNTLTKPEISDTRIGAVOYT 540
QY 541 YEOGLEFGPKYSSKPDILNAIKRVGWSSGTSFGAINFLEQLFKSKRKNKMLILI 600
Db 541 YEOGLEFGPKYSSKPDILNAIKRVGWSSGTSFGAINFLEQLFKSKRKNKMLILI 600
QY 601 TDGGSYDVRIPMAAHLKGVITTAIGVAAAOELEVIAIHPARDHSFVDEFDNLHOY 660
Db 601 TDGGSYDVRIPMAAHLKGVITTAIGVAAAOELEVIAIHPARDHSFVDEFDNLHOY 660
QY 661 VPRITONICTEFNSOPRN 678
Db 661 VPRITONICTEFNSOPRN 678

RESULT 2
Q9UDNO HUMAN PRELIMINARY; PRT; 693 AA.
AC Q9UDNO: Q96DW8;
DT 01-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 2.
DE Hypothetical protein VIT (Hypothetical protein FLJ32210).
GN Name=VIT;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo;
OX NCBI_TaxID=9606;
RN [1]
RA Nucleotide sequence.
RA Cordes M., Kalicki J., Ames M.;
RT "The sequence of Homo sapiens BAC clone Rp11-29411.",
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RA Nucleotide sequence.
RA Waterston R.H.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RA Nucleotide sequence.
RA Waterston R.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

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RN [4]
RP Nucleotide sequence.
RA Wilson R.X.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RN [5]
RP Nucleotide sequence.
RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura T., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto Y., Saito K., Kawai Y., Isono Y., Nakamura Y., Negahari K.,
RA Muzakami K., Yaeda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hobori T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M., Yamazaki M.,
RA Niimura K., Iehibashi T., Yamashita H., Murakami K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Iehida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hozuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yonki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshihawa Y., Matsunawa H., Ichihara T., Shibahara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Hishigaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujitawa T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kanabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtsuki K., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maeno H., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
CC
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CC
CC EMBL: AK056772; BAB71279.1; -; mRNA.
CC EMBL: AC007363; AAF19243.2; -; genomic_DNA.
CC
CC HSSP: O43405; IJBI.
CC
CC HGNC: HGNC:12697; VIT.
CC InterPro: IPR004043; LCCL.
CC InterPro: IPR002035; VWF_A.
CC Pfam: PF03815; LCCL. 1.
CC Pfam: PF00092; VMA; 2.
CC PRINTS: PR00453; VWFADOMAIN.
CC SMART: SM00603; LCCL. 1.
CC SMART: SM00327; VMA; 2.
CC PROSITE: PS50820; LCCL. 1.
CC PROSITE: PS50234; VWF; 2.
CC KX Hypothetical protein.
SQ
SEQUENCE 693 AA; 75575 MW; 2DEBB2421F2D496D CRC64;

Query Match 99.5%; Score 3484.5; DB 2; Length 693;
Best Local Similarity 97.8%; Pred. No. 4.3e-218; Indels 15; Gaps 1;
Matches 678; Conservative 0; Mismatches 0;

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Db      121 VOSLSLPMWRSEFVLESKPKKGVTPSPALTYSSSSKSPAAGETTKAYQRPPIGTTAQ 180
Qy      181 PVTLMQLLAVTAAVATPTTLPRPSPAASTTSIPRPOSGHRSQEMDLMSTATYSSQNR 240
Db      181 PVTLMQLLAVTAAVATPTTLPRPSPAASTTSIPRPOSGHRSQEMDLMSTATYSSQNR 240
Qy      241 PRADPGIORQDPSGAFAQKPVGADVSL-----GLVPEKEELSTQSLSPVSL 285
Db      241 PRADPGIORQDPSGAFAQKPVGADVSLGEMDSWKPGSVLLDEGLVPKEELSTQSLSPVSL 300
Qy      286 GDPNCKIDSLFLIDSTSGKRRFRIOKQLLDVAQALDIPAGPLMGVVOYGDNPATHF 345
Db      301 GDPNCKIDSLFLIDSTSGKRRFRIOKQLLDVAQALDIPAGPLMGVVOYGDNPATHF 360
Qy      346 NLKHTNSRDLKTAIEKTORGGLSNVGRAISFTVKNFPSKANGNSGAPNVVVVWDGM 405
Db      361 NLKHTNSRDLKTAIEKTORGGLSNVGRAISFTVKNFPSKANGNSGAPNVVVVWDGM 420
Qy      406 PTDKVEASRLARESGINIFITIEGAANEKQYVVEPNFANKAVCRTNGFYSLHVQSWF 465
Db      421 PTDKVEASRLARESGINIFITIEGAANEKQYVVEPNFANKAVCRTNGFYSLHVQSWF 480
Qy      466 GLHKTLOPLVRCVCTDBLACSKTCLNSADIGFVIDSSSVGTGNFRITVLOFVTMLTKBF 525
Db      481 GLHKTLOPLVRCVCTDBLACSKTCLNSADIGFVIDSSSVGTGNFRITVLOFVTMLTKBF 540
Qy      526 EISPTDRIGAVOYVTEOERLEFPDKYSSKPDILNAIKRVGWSGTSFGAALNFALBOL 585
Db      541 EISPTDRIGAVOYVTEOERLEFPDKYSSKPDILNAIKRVGWSGTSFGAALNFALBOL 600
Qy      586 FKSKPNRKLMIITDGRSYDDVRIPMAAHLKGVITTAIGVMAAOEELVIAITHPAR 645
Db      601 FKSKPNRKLMIITDGRSYDDVRIPMAAHLKGVITTAIGVMAAOEELVIAITHPAR 660
Qy      646 DHSFVDFEFDNLHQVPRRIQNICTEFNSOPRN 678
Db      661 DHSFVDFEFDNLHQVPRRIQNICTEFNSOPRN 693

RESULT 3
ID      096DT1_HUMAN      PRELIMINARY;      PRT;      656 AA.
AC      096DT1;
DT      01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT      01-DEC-2001, sequence version 1.
DT      07-FEB-2006, entry version 16.
DE      Victim.
GN      Name=VIT;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC      Homo
NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=skeletal muscle;
RA      Ren Z.-X., Liu J.G., Mayne R.;
RL      Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC      -----
EMBL: AF063833; AAL18263.1; -. mRNA.
DR      HSSP; O43405; IJBI
DR      InterPro; IPR004043; LCCL
DR      InterPro; IPR02035; VWF_A
DR      Pfam; PF03815; LCCL; 1.
DR      Pfam; PF00092; VMA; 2.
DR      PRINTS; PR00453; VWFADOMAIN.
DR      SMART; SM00603; LCCL; 1.
DR      SMART; SM00327; VMA; 2.
DR      PROSITE; PS50820; LCCL; 1.
DR      PROSITE; PS50234; VMA; 2.

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SQ      SEQUENCE      656 AA;      71768 MW;      E242E00DEB07CF2C CRC64;
Query Match      95.5%;      Score 3344;      DB 2;      Length 656;
Best Local Similarity 96.0%;      Pred. No. 5.7e-209;
Matches 651;      Conservative 1;      Mismatches 4;      Indels 22;      Gaps 1;

Qy      1 MRTVLTNKAIVIEFLVLTGVHNSKETAKIKRPRTVPOINCADVAKIIDPEFV 60
Db      1 MRTLVTNKAIVIEFLVLTGVHNSKETAKIKRPRTVPOINCADVAKIIDPEFV 60
Qy      61 KCPACQDPKHYVTDVYASISYVCGAAVHSVGLDNGSGKITLVKVAQSGSYKSYNG 120
Db      61 KCPACQDPKHYVTDVYASISYVCGAAVHSVGLDNGSGKITLVKVAQSGSYKSYNG 120
Qy      121 VOSLSLPMWRSEFVLESKPKKGVTPSPALTYSSSSKSPAAGETTKAYQRPPIGTTAQ 180
Db      121 VOSLSLPMWRSEFVLESKPKKGVTPSPALTYSSSSKSPAAGETTKAYQRPPIGTTAQ 180
Qy      181 PVTLMQLLAVTAAVATPTTLPRPSPAASTTSIPRPOSGHRSQEMDLMSTATYSSQNR 240
Db      181 PVTLMQLLAVTAAVATPTTLPRPSPAASTTSIPRPOSGHRSQEMDLMSTATYSSQNR 240
Qy      241 PRADPGIORQDPSGAFAQKPVGADVSLGLVPEKEELSTQSLSPVSLGDPNCKIDSLFLIDG 300
Db      241 PRADP-----GLVPEKEELSTQSLSPVSLGDPNCKIDSLFLIDG 278
Qy      301 STSIGKRRFRIOKQLLDVAQALDIPAGPLMGVVOYGDNPATHPNLKHTNSRDLKTAI 360
Db      279 STSIGKRRFRIOKQLLDVAQALDIPAGPLMGVVOYGDNPATHPNLKHTNSRDLKTAI 338
Qy      361 EKTORGSLNVGRAISFTVKNFPSKANGNSGAPNVVVVWDGPTDKVEASRLARES 420
Db      339 EKTORGSLNVGRTISTFTVKNFPSKANGNSGAPNVVVVWDGPTDKVEASRLARVS 398
Qy      421 GINIFITIEGAANEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLOPLVRCVCD 480
Db      399 GINIFITIEGAANEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLOPLVRCVCD 458
Qy      481 TDBLACSKTCLNSADIGFVIDGSSSVGTGNFRITVLOFVTMLTKFEISDTRIGAVOYT 540
Db      459 TDBLACSKTCLNSADIGFVIDGSSSVGTGNFRITVLOFVTMLTKFEISDTRIGAVOYT 518
Qy      541 YEORLEFGFDKYSSKPDILNAIKRVGWSGTSFGAALNFALBOLFKSKPNRKLMIILI 600
Db      519 YEORLEFGFDKYSSKPDILNAIKRVGWSGTSFGAALNFALBOLFKSKPNRKLMIILI 578
Qy      601 TDGRSYDDVRIPMAAHLKGVITTAIGVMAAOEELVIAITHPARDSFFVDFEFDNLHQY 660
Db      579 TDGRSYDDVRIPMAAHLKGVITTAIGVMAAOEELVIAITHPARDSFFVDFEFDNLHQY 638
Qy      661 VPRRIQNICTEFNSOPRN 678
Db      639 VPRRIQNICTEFNSOPRN 656

RESULT 4
ID      03T247_MOUSE      PRELIMINARY;      PRT;      650 AA.
AC      03T247;
DT      11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT      11-OCT-2005, sequence version 1.
DT      07-FEB-2006, entry version 5;
DE      Adult inner ear cDNA, RIKEN full-length enriched library,
DE      clone: F930032K14 product: vitrin, full insert sequence.
GN      Name=VIT;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=inner ear;

```

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=inner ear;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodius R., Shimokawa K.,
 RA Davis M.J., Wilson L.G., Aldine V., Allen J.E.,
 RA Amesni-Imbriaco A., Apweiler R., Auraliya R.N., Bailey T.L.,
 RA Bansal K.P., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 RA Chiu K.P., Choudhary V., Christofels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Gestblom S., Harbers M., Hayashi Y., Henich T.K., Hirokawa N.,
 RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mutsaers J., Taber S., Mulder N., Nakano N., Nakachi H., Ng P.,
 RA Nilsen R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlowski V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J.C., Reid J.F., Ring B.Z., Ringwald M.,
 RA Roat B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Sperling S., Stupka E., Sugita K., Sulana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeig K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hilde W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Matlock J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Karayama M., Suzuki M., Aoki J., Arikawa T.,
 RA Iida Y., Imanura K., Itoh M., Kato T., Kawai H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=inner ear;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RA RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=inner ear;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nishikido I., Osato N., Saito R., Suzuki H., Yamashita I., Kiyosawa H.,
 RA Yeig K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake U.A., Bratt D., Brucic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kiyosawa A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Matsuda H., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Petia G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yamanishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=inner ear;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamashita I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nishikido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita R., Tomita M., Wagner L.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barz G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bono B.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaeets P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto S.,
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=inner ear;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=inner ear;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishitani T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Ozawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Maruwa S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multiplexed sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=inner ear;
 RA Arikawa T., Carninci P., Fukuda S., Hashizume M., Hayashida K.,
 RA Hori F., Iida Y., Imanura K., Imutani K., Itoh M., Kanagawa S.,
 RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
 RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
 RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.


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Db      450 VCDTRDLACSKTCLNSADIGFVIDGSSSVGTSNFRVYQFVANI.SKEFEIDDTDRVGA 509
Qy      538 QYTEORLEFEGFDKSSKPDILNIAIKRVYWSGGSTGAALNFALEOLF.KSKSKPKRKLTM 597
Db      510 QYTEORLOFDFDKNSKADILSLAIRVYWSGGSTGAALQYALEOLF.KSKSKPKRKLTM 569
Qy      598 ILITDGRSYDDVRIPAMAAHLKGVITTYAIGVMAAOEELVIAITHPARDSFFVDEPDL 657
Db      570 IITDGRSYDDVRIPAMAAHQGVITTYAIGVMAAOEELVIAITHPARDSFFVDDPDL 629
Qy      658 HQYVPRITONICTEPNSOPRN 678
Db      630 YKIAPRIIONICTEPNSOPRN 650

RESULT 6
Q95LI2_BOVIN PRELIMINARY; PRT; 652 AA.
ID Q95LI2_BOVIN PRELIMINARY; PRT; 652 AA.
AC Q95LI2
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 2.
DT 07-FEB-2006, entry version 16.
DE Vitrin.
GN Name=VIT;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RA Ren Z.-X., Liu J.G., Mayne R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; AF063832; AAL18262.2; -, mRNA.
DR HSSP; O43405; IJBI.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VWA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWF_A; 2.
SQ SEQUENCE 652 AA; 70873 MW; 3512421CA6987C51 CRC64;

Query March 80.5%; Score 2818; DB 2; Length 652;
Best Local Similarity 79.8%; Pred. No. 1e-174;
Matches 541; Conservative 49; Mismatches 62; Indels 26; Gaps 2;

Qy      1 MRLVLTLMKASVIMFLVLTGVSNNKETAKKIKRPFYVPOINCDVAKGIIDPEFIV 60
Db      1 MGIVLTMKASVIMFLVLTGVSNNKETAKKIKRPFYVPOINCDVAKGIIDPEFIV 60
Qy      61 KCPAGCCDPRHYVGVADYVASSYSCGAHVHSGVLDNSGGKILVRKAVAGSGYKGSYNG 120
Db      61 KCPAGCCDPRHYVGVADYVASSYSCGAHVHSGVLDNSGGKILVRKAVAGSGYKGSYNG 120
Qy      121 VQSLSLPRMRSEFVLESKPKKGVITYPSALTYSSSKSPAAGETTXAYORPPIPGTAAQ 180
Db      121 VQSLSLPRMRSEFVLESKPKKGVITYPSALTYSSSKSPAAGETTXAYORPPIPGTAAQ 180
Qy      181 PVTYVQAQPGTAAIATHTTLTKPKSPSAGSTASGARPGAPGAKRMDL----- 226
Db      181 PVTYVQAQPGTAAIATHTTLTKPKSPSAGSTASGARPGAPGAKRMDL----- 226
Qy      241 PRADPGIGRQDPSGAAROKPVGADVSLGLVPEKEILSTOSLEPVLGDPNCKIDLSFLIDG 300

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Db      227 --GEP-----AAMKESVLLDAGFVPEKELSTQSLSPASQGPSCKVDLSFLIDG 274
Qy      301 STSICKRRFRLOKOLLADVQAOLDIGPAGPLMGVVOYGDNDPAPATHFNKLTNTSBDLTAI 360
Db      275 SSSIGKRRFRLOKOLLADVQAOLDIGPAGPLMGVVOYGDNDPAPATHFNKLTNTSBDLTAI 334
Qy      361 EKITQRGSLSNVGRALISFVTKNFSSKANGRSGAPNVVVMVDGMPDTRKYEASRLARES 420
Db      335 EKISQRGSLSNVGRALISFVTKNFSSKANGRSGAPNVVVMVDGMPDTRKYEASRLARES 394
Qy      421 GINIFFTITGAANEQYVVEPFAKVAICRTNGFSLVQSGFGLHKTLOPLVXVCD 480
Db      395 GVINIFFTITGAANEQYVVEPFAKVAICRTNGFSLVQSGFGLHKTLOPLVXVCD 454
Qy      481 TDRLACSKTCLNSADIGFVIDGSSSVGTSNFRVYQFVNI.LKXFEISDTRIGAVOYT 540
Db      455 TDRLACSKTCLNSADIGFVIDGSSSVGTSNFRVYQFVNI.LKXFEISDTRIGAVOYT 514
Qy      541 YEORLEFEGFDKSSKPDILNIAIKRVYWSGGSTGAALNFALEOLF.KSKSKPKRKLMI 600
Db      515 YEORLEFEGFDKSSKPDILNIAIKRVYWSGGSTGAALNFALEOLF.KSKSKPKRKLMI 574
Qy      601 TDGRSYDDVRIPAMAAHLKGVITTYAIGVMAAOEELVIAITHPARDSFFVDEPDLHQY 660
Db      575 TDGRSYDDVRIPAMAAHLKGVITTYAIGVMAAOEELVIAITHPARDSFFVDEPDLHKV 634
Qy      661 VPRITONICTEPNSOPRN 678
Db      635 VPRITONICTEPNSOPRN 652

RESULT 7
Q8K047_MOUSE PRELIMINARY; PRT; 650 AA.
ID Q8K047_MOUSE PRELIMINARY; PRT; 650 AA.
AC Q8K047
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Vitrin.
GN Name=Vlt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien M., Soares M.B., Bonaldo M.F., Casavant T.B., Schaefer C.F.,
RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Farey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;

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Db 330 TAIEKTORGGLSNVGRASIFFTKTFEFGKANGNRCGANVAVVWDGPTDKVEEVSRYA 389
 Qy 418 RESGNIFPITIEGAENEKQVYVPEANFANKVCTNGFYSIHNQSGMGLHKTLOPLVKR 477
 Db 390 RESGNVFFITVEGAERDIOHVEPGASAKVCTNGFYSFNQSGMGLHKTVOPLVKR 449
 Qy 478 VCDPDRRLACSKTCLNSADIGFVIDSSVGTGNFRTVQFVNLKFEFISDTRIGAV 537
 Db 450 VCDPDRRLACSKTCLNSADIGFVIDSSVGTGNFRTVQFVNLKFEFISDTRIGAV 509
 Qy 538 QYTYEQRLEFPGFDKXSKPDILMAIKRVGVSGTSTGAALNFALEQLFKSKPKRKLK 597
 Db 510 QYTYEQRLEFPGFDKXSKPDILMAIKRVGVSGTSTGAALNFALEQLFKSKPKRKLK 569
 Qy 598 ILITDGRSDYDVRIPAMAAHKGVTYTAIGVMAAOELEVYATHTPADHSFVDEPNTL 657
 Db 570 ILITDGRSDYDVRIPAMAAHKGVTYTAIGVMAAOELEVYATHTPADHSFVDEPNTL 629
 Qy 658 HQVPRRIQNICTEFNSOPRN 678
 Db 630 YKIPRIQNICTEFNSOPRN 650

RESULT 9

Q8BQ41 MOUSE PRELIMINARY; PRT; 628 AA.
 ID Q8BQ41_MOUSE
 AC Q8BQ41_MOUSE
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 19.
 DE 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched
 DE library, clone: D130059M21 product: VIRININ homolog.
 GN Name: vit;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC NCBI_Muridae; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Katagawa T., Katayama S., Gough J., Frich M.C., Maeda N.,
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Balic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impollato A., Apweiler R., Auraliysa R.N., Bailey T.L.,
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 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
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 RA Kitano H., Kohlas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
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 RA Ljung S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottacchi-Traber S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,

RA Schonbach C., Sekiguchi K., Sempke C.A., Seno S., Seesla L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 RA Spelling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
 RA Yamanishi H., Zdobovskiy E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wallestedt C., Matick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imanura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the PANTOM Consortium;
 RT "Antisense transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nishikido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirini L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Giustolisi S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Namata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wallestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hata A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Iwama M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochawa H.,
 RA Kuohi P., Lewis S., Matsuo Y., Nishikido I., Pesole G., Quackenbush J.,
 RA Schirini L.M., Straub J.F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barin G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Giustolisi S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Schoenwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayaishi Y.,
RT "Functional annotation of a full-length mouse cDNA collection";
RT Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA Aachti U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hasegaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
RA Horii F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawachi J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kishihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL: AK051606; BAC34688.1; -; mRNA.
CC
CC HSSP: O43405; 1JBI
CC
CC Ensembl: ENSMUSG00000024076; Mus musculus.
CC
CC MGI: MGI:1921449; V1C.
CC
CC GO: GO:0005615; C:extracellular space; RCA.
CC
CC InterPro: IPR004043; LCCL.
CC
CC InterPro: IPR002035; VWF_A.
CC
CC Pfam: PF03815; LCCL, 1.
CC
CC Pfam: PF00092; VMA, 2.
CC
CC PRINTS: PR00453; VMPADOMAIN.
CC
CC SMART: SM00603; LCCL, 1.
CC
CC SMART: SM00327; VMA, 2.
CC
CC PROSITE: PS50820; LCCL, 1.
CC
CC PROSITE: PS50234; VMA, 2.
CC
CC SQUENCE 628 AA; 68198 MW; C96C4ACE9E72480 CRC64;
SO

Query Match 76.6%; Score 2682; DB 2; Length 628;
Best Local Similarity 77.7%; Pred. No. 7, 1e-16;
Matches 529; Conservative 39; Mismatches 57; Indels 56; Gaps 6;

QY 1 MRRVVLTKRSKSVEMFLVLVTGVHSNKETAKKIKRKFYVPOINCVKAGKIIDPEFIY 60
DB 1 MGIWPTMKASVLEVL-----AVPQINCVDKAGKIINPEFMV 38

QY 61 KCPAGCDDPKHYVGTDVASYSVCGAAVHSGVLDSGKILVRKAGOGYKGSYNG 120
DB 39 KCPAGCDDPKHYVGTDVASYSVCGAAVHSGVLDSGKILVRKAGOGYKGSYNG 98
QY 121 VQSLSPRMRBSFVLESKPKKGVTPYSALTYSSSKSPAQAAGETTYAYORPPIEGTTAQ 180
DB 99 VQSLSPRMRBSFVLESKPKKGVTPYSALTYSSSKSPAQAAGETTYAYORPPIEGTTAQ 158
QY 181 PVTLMQLLATVNAVATPTLPRPSPASSTSTPRPOSVGHRSQEM---DLMSATVYTS 237
DB 159 PVTLMQLLATVNAVATPTLPRPSPASSTSTPRPOSVGHRSQEM---DLMSATVYTS 209
QY 238 QNRPRADPGIORQDPSGAARQPGADVSLGLVPEKELSTOSLEPVSIGDPNCKIDLSFL 297
DB 210 -----PG-----PVLDD--SGFVPEKELSTOSLEPVSIGDPNCKIDLSFL 247
QY 298 IDGSTSGKRRFRIOKQLADVAQALDIPAGPLMGVVOYGDNPATHTFNLTHTNSRDLK 357
DB 248 IDGSTSGKRRFRIOKQLADVAQALDIPAGPLMGVVOYGDNPATHTFNLTHTNSRDLK 307
QY 358 TALEKTORGSLNVGSAISFVTKNPFSSKANGRSGAPNVVMMVDDGPTDKYEBASRLA 417
DB 308 TALEKTORGSLNVGSAISFVTKNPFSSKANGRSGAPNVVMMVDDGPTDKYEBASRLA 367
QY 418 RESGINIFTTIEGAENKQYVVEPNFANKAVCRTNGFYSLSHVQSWFGHLTKLOPLVKR 477
DB 368 RESGINIFTTIEGAENKQYVVEPNFANKAVCRTNGFYSLSHVQSWFGHLTKLOPLVKR 427
QY 478 VCDTRDLACSKTCLNSADIDGFVIDGSSVGTGNFRYVLOVYTNLTKEFELSDPTRGAV 537
DB 428 VCDTRDLACSKTCLNSADIDGFVIDGSSVGTGNFRYVLOVYTNLTKEFELSDPTRGAV 487
QY 538 QYTEQGLEFGPKYSKPDILNAIKRVGWSGTSGAALNPALEQTFPKSKPNKSKLM 597
DB 488 QYTEQGLEFGPKYSKPDILNAIKRVGWSGTSGAALNPALEQTFPKSKPNKSKLM 547
QY 598 ILITDGSYSDVRIIPAMAAHKGITTYAIGVAAAQOELEVIATHPARDSFVDEPDL 657
DB 548 ILITDGSYSDVRIIPAMAAHKGITTYAIGVAAAQOELEVIATHPARDSFVDEPDL 607
QY 658 HQYVPRITQICTEFNSQPN 678
DB 608 YKIAFRITQICTEFNSQPN 628

RESULT 10
Q5NTW9_CHICK PRELIMINARY; PRT; 748 AA.
AC Q5NTW9;
DT 01-FEB-2005, integrated into UniProtKB/TREMBL.
DT 01-FEB-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Aklirin precursor.
GN Name=Aklirin;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15765510; DOI=10.1002/dvdy.20303;
RA Ahsan M., Ohta K., Kuriyama S., Tanaka H.;
RT "Novel soluble molecule, Aklirin, is expressed in the embryonic chick
RT eyes and exhibits heterophilic cell-adhesion activity";
RL Dev. Dyn. 233:95-104(2005).
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CC
CC EMBL: AB185956; BAD81032.1; -; mRNA.
CC
CC InterPro: IPR004043; LCCL.

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DR InterPro; IPR02035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VMA; 2.
DR Signal.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 748 AA; 81400 MW; 16299BFCDF85F70E CRC64;

Query Match 66.0%; Score 2311.5; DB 2; Length 748;
Best Local Similarity 60.4%; Pred. No. 1,2e-141;
Matches 457; Conservative 86; Mismatches 120; Indels 93; Gaps 8;

QY 8 MKASVIEFELVLTGVHSNKEETAKIKRPKFTVPQINCVDYAKKIIDPEFIYKCPACQ 67
DB 1 MKASVIATFFGVLLTCTVAAKEATKTKKAEIYIPQIDCDVYAGKIIINPEFIACPCQ 60
QY 68 DPKHYVGTDVYAYSVCSGAHVSGVLNDGSGKILYKRVAGSGSGYKSGYNGVLSLP 127
DB 61 DVKTRVGTDIYAFSSACSAHSGAIDNTGSKILVQKVGHAGYRGSFSGVRSLSLP 120
QY 128 RMRESFVLESKPKKGVTPSPALTYSSSKSPA----- 160
DB 121 RMRSFVSEKPKKGVTPSPALTYSSSKSPA----- 160
QY 121 RMRSFVSEKPKKGVTPSPALTYSSSKSPA----- 160
DB 121 RMRSFVSEKPKKGVTPSPALTYSSSKSPA----- 160
QY 161 QAGETT-KAYGRPPIPGTTAQPVTLMQLAVTAVATPT-----TLRPSPSAASTSI 213
DB 181 EQGTVRKVYQTSFVPMPTTQ-----MAATTPPTTTTDDPSTKPTTTPATPTT 233
QY 214 -----PRP-----QSNGRQEMDLMSTATYSSQ 238
DB 234 TDSAAAKRPQLQVRDTGSSVHPAYSSVAAAAROVQAGRGKLNKAFRGSTTSASNR 293
QY 239 NRPPADPGIQRODPSGAFOKPVGADVSL-----GLVPKEELSTQSLER 282
DB 294 NILRPNAGIQOQEPV-ATVRRPAGSPALHAIETDLMKRGSPFDGFGASKELNKLPEA 352
QY 283 VSLDPPNCKIDLSPILIDGSTSIGKRFRIOQLADVQAOLDIGPAGFLMGVVOYGDNP 342
DB 353 TSQGNPSCKVDLPFLMDGWSIGKRFPOLQOKFLINVAHAGINNAGLMTGIVQYGDPS 412
QY 343 THENLKTHTNRDLKTAIEKITTQCGSLNNGRAISFVTKNPFSSKNGRSGAPNYYVMV 402
DB 413 TEFNLKTYASPEKELRNALIEKIPOKGLSNVGKALSFNKPFPSDNGNRGAPNYYVMV 472
QY 403 DGMFTDKVEEASRLARESGINIFFTIGAAENKQYVVEPNFANKAVCRTNGFYSLHVQ 462
DB 473 DGMFTDKVEEASRLARESGINIFFTITPAADQNEKQVIEENFVDKAVCRNNGFYSIVP 532
QY 463 SWPGLAKTLQPLVXKVCPTDRLACSKTCLNSADIGFVIDGSSSVGTGFRVLOFVNL 522
DB 533 SWPGLAKTLQPLVXKVCPTDRLACSKTCLNSADIGFVIDGSSSVGTGFRVLOFVNL 522
QY 523 KEFISIDPTDRIIGAIQYVEQLREPSFDKYSTKQDVLSAIRINWSSGCTGGAISTAS 652
DB 593 KEFISIDPTDRIIGAIQYVEQLREPSFDKYSTKQDVLSAIRINWSSGCTGGAISTAS 652
QY 583 EQLPKSKPKRKMILITDGRSYVDVRI PAMAALHKLGVITYAIGVAAAQEELEVIAT 642
DB 653 EQLPKSKPKRKMILITDGRSYVDVRI PAMAALHKLGVITYAIGVAAAQEELEVIAT 642
QY 643 PARDHSFVDFEDNLHQYVPRIIIONICTEENSOPRN 678
DB 713 PDKESHFVDFEDNLHQYVPRIIIONICTEENSOPRN 678

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RESULT 11
QARP27-TESTNG PRELIMINARY; PRT; 680 AA.
AC QARP27;

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DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 17 SCARF15006, whole genome shotgun sequence. (Fragment).
GN ORFNames=STENG00030857001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OK NCBI_Taxid=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Strange-Thomann N.,
RA Maucel E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicod S., Jaffe D., Fisher S., Lutfalla G., Dobet C., Segurens B.,
RA Daehli V., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Giraud C., Duprat S., Brottier P., Couanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Queller F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Reest Crolius H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RI Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; CAB01015006; CAG09535.1; -; Genomic_DNA.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR02035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VMA; 2.
FT NON TER
SQ SEQUENCE 680 AA; 74841 MW; E6B866AF3A17C1A6 CRC64;

Query Match 55.1%; Score 1929; DB 2; Length 680;
Best Local Similarity 56.5%; Pred. No. 8,9e-117;
Matches 393; Conservative 86; Mismatches 145; Indels 70; Gaps 10;

QY 37 PKFTVPQINCVDYAKKIIDPEFIYKCPACQDPRHYVGTDVYASVCSGAHVSGVLD 96
DB 1 PSAVIPALIECDVRGKINLPFIKCPHCKESQOYVGTVGFVASTISICNAALHSGVIT 60
QY 97 NSGKILYKRVAGSGYKSGYNGVLSLPRMRESFVLESKPKKGVTPSPALTYSSSK 156
DB 61 NAGKIVYKRVAGSGYKSGYNGVLSLPRMRESFVLESKPKKGVTPSPALTYSSSK 120
QY 157 SPAAQAGT-TKAYGRPPIPGTTAQPVTLMQLAVTAVATPTTLP-----RSPSAS 209
DB 121 PTYVKTSETRLEVY-----IOKDAKSLAAAVTRTLPMLLQVQSHKAK 165
QY 210 TTSLPRQSVGRQEMDLMSTATYSS-----Q 238
DB 166 EVVPKAPLSGDNHLLDQVSLSYTHTHLHTRSKNPGDRKXFFGSGGRLPVRRPQ 225

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QY 239 NRP--RADPGIQRDPGSAF---QKPYGADV-----SLGVPEKEELSTQSLPEVSL 285
 Db 226 QRPYSQATGWDHDIIP-GCVAFASQKGLGPFVPRSPPTTSIKFFLQGFAPSSSLTSLRA 284
 QY 286 GDP-NCKTIDSLFLDSTSTGKRRFRITOKLLAVQAALDIPGAPPLMGVQYQDNPRTH 344
 Db 285 DHPPECCKIDLVFLMDGWSIGKRRFKIQKDLAEVAQAIVNGPTGPMGVQYQDVPYTE 344
 QY 345 FNLKTHNSRDLKTAIEKITQRGGLSNVGRASIFVTNKFPSKANGNSGAPNVVVMYDG 404
 Db 345 ISLKSVSSSSRKARAAVEKITQKGLSHVGRALSTYNNQYFSDANGNKAANNAVAVLDG 404
 QY 405 WPTDKVEASRLARESGINIFITIEGAENKQYVEPNPANKAVCTNGSFYSLHVQSW 464
 Db 405 WPTDKVEASRLARESGINIFITIEGPDLEKQKVHEHDFVDKAVCTSGFSFSLPVSSW 464
 QY 465 FGLHKTLOPLVKRCVCDTRLACSKTCLNSADIGVTDGSSSVGNGNPRVTUQPTNLTK 524
 Db 465 FALRKVLQPLVKRCVCDTRLVCSKTCLNANDIAFVIDGSSSVGNGNPRVTUQPTNLTK 524
 QY 525 FEISDTRIGAVQYTYEORLEFGFDKYSKRPDLINAIKRVYSGSGTGAALNFALEQ 584
 Db 525 FEISDTRIGAVQYTYEORLEFGFDKYSKRPDLINAIKRVYSGSGTGAALNFALEQ 584
 QY 585 LFKKSKENKRLMLITDGRSYDDVRIPAMAHLKGVITTAI--GVANAAQELLEVIATH 642
 Db 585 LFSSKSKENKRLMIVITDGRSYDDVRIPAAVHROGQCHDLRGLHRAWAODELEVIATD 644
 QY 643 PARHSEFVDEFDNLHOVPRITONICTEFPNSOPRN 678
 Db 645 PDAHSEFVDEFDNLKRFVPRIVSNICOEFNSOPRN 680

RESULT 12

Q8AM56_BRAE PRELIMINARY; PRT; 553 AA.
 AC Q8AM56;
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Novel protein similar to human coagulation factor C homolog (Cochlin, COCH).
 GN Name=Coch; Synonyms=OTTDAHP0000001491; ORFNames=d2234G15.4-001;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCBI_TaxID=7935;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Babbage A.;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
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 DR EMBL; AL596026; CAD58748.1; -; Genomic_DNA.
 CC HSSP; 043405; 1JBI.
 DR HSSP; ENSDARG00000024032; Danio rerio.
 DR ZFIN; ZDB-GENE-030616-403; coch.
 DR InterPro; IPR004043; LCCL.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF03815; LCCL.1.
 DR Pfam; PF00092; VMA.2.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00603; LCCL.1.
 DR SMART; SM00327; VMA.2.
 DR PROSITE; PSS0820; LCCL.1.
 DR PROSITE; PSS0234; VMA.2.
 SO SEQUENCE 553 AA; 60351 MW; 4A3B136747C488F0 CRC64;

Query Match 33.9%; Score 1187.5; DB 2; Length 553;
 Best Local Similarity 37.7%; Pred. No. 1.3e-68;

Matches 251; Conservative 107; Mismatches 184; Indels 123; Gaps 8;
 QY 16 FLVLLVTGVH-----NKEAKKIKRPFVPOINCVDKAKIIDPEFIVKCPAGCOPPKY 71
 Db 5 PAVLVHVGIIISLCKTSGSELNATP-----ISCGRAVDLDELTHLVLCPRNCSLSL 58
 QY 72 HVGTDVYASYSVCGAAVHSGVLDSGKILYRKVAGSGGYSNGYQSLSLPWRE 131
 Db 59 SVFSGGYVASISSICGAAIHRIIGISGCPVEVHGLQGRNTYSSVHAGVQSLSQWSA 118
 QY 132 SFVLEKPKKGYTPALTYSSSKSPAAGETTYAKQRPPIGTTAQVTLMQLAVT 191
 Db 119 SF----- 120
 QY 192 VAVATPTLPRPSPAASITSIIPRQSVGRSQSMDLMTATYTSQNRBRADPGIOROD 251
 Db 121 -TVARTISLLEVSSQYSSSAIV----- 142
 QY 252 PSGAAGKPYGADVSLGLVPEKEELSTQSLPEVSGDPNCKIDSLFLDSTSGKRRFR 311
 Db 143 ASGAA-KKPYKK-----IVKK-----PPATAHKDCVDMAALLDSSYNIQORFNL 188
 QY 312 QKQLADVQAALDIPGAPPLMGVQYQDNPRATHFNLKTHNSRDLKTAIEKITQRGSLN 371
 Db 189 QKQNVSKLATMLKVGITQGPVHGVQTSERTPTETLTNTYTAQVFAIKETPIGNTN 248
 QY 372 VGRAISFVTNKFPSKANGNSGAPNVVVMVWDGPTDKVEASRLARESGINIFITIEG 431
 Db 249 TGRALHTVANNFSPDPGVARGYPRIIVVFDGMPDSNVBEAAILARESGINIFPVSAK 308
 QY 432 AAENKQYVEPNPANKAVCTNGSFYSLHVQSWFGLHKTLOPLVKRCVCDTRLACSKTCL 491
 Db 309 PSPEASLVSDDQDFMRKAVCKDNEFFFTPTPSWFSTKFKVPLQKCSIDOMLCKTCY 368
 QY 492 NSADIGFVTDGSSSVGNGNPRVTUQPTNLTKFEISDTRIGAVQYTYEORLEFGFDK 551
 Db 369 NSVDLGFLLDSSSVGNGNPRVTUQPTNLTKFEISDTRIGAVQYTYEORLEFGFDK 428
 QY 552 YSSKPDILNAIKRVYSGSGTGAALNFALEQLFKSKENKRLMLITDGRSYDDVR 611
 Db 429 HVLKDNMLRLQKIPYWSGATGDAINFVRLSKFRSSNNKFLIITDGRSYDDVR 488
 QY 612 PAMAHLKGVITTAIYVAMAAQELLEVIATHPARHSEFVDEFDNLHOVPRITONIC-- 669
 Db 489 PAMAAGREGITVAVGAMAPMEDLKAMSEPKESHVFRTFEPTGLGFOQPIVIGICRD 548
 QY 670 -TEFN 673
 Db 549 FTEFN 553

RESULT 13

COCH_CHICK STANDARD; PRT; 547 AA.
 AC 042163;
 DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
 DT 01-JAN-1998, sequence version 1.
 DT 07-FEB-2006, entry version 39.
 DE Cochlin precursor (COCH-SB2).
 GN Name=COCH; Synonyms=COCHSB2;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA], TISSUE SPECIFICITY, AND DEVELOPMENTAL
 RP STAGE.
 RC STRAIN=White leghorn; TISSUE=Basilar papilla;
 RX MEDLINE=98409669; Pubmed=9736748; DOI=10.1073/pnas.95.19.11400;
 RA Heller S., Sheane C.A., Javed Z., Hudspeth A.J.;
 RT "Molecular markers for cell types of the inner ear and candidate genes
 for hearing disorders.";


```

RL Proc. Natl. Acad. Sci. U.S.A. 95:11400-11405(1998).
CC -1- SUBCELLULAR LOCATION: Secreted protein (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in inner ear structures: the
CC spiral-shaped cells of the basilar papilla. Weaker expression
CC found in the inferior and superior fibrocartilaginous plates and
CC skeletal muscle.
CC -1- DEVELOPMENTAL STAGE: Specifically expressed at the late
CC developmental stages in the cochlea.
CC -1- SIMILARITY: Contains 1 LCCL domain.
CC -1- SIMILARITY: Contains 2 WMFA domains.
CC -1- DATABASE: NAME=Protein Spotlight; NOTE=Issue 4 of November 2000;
CC WWW="http://www.expasy.org/spotlight/back_issues/split004.shtml".
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL; AF012252; AAC62253.1; -, mRNA.
DR HSSP; O43405; 1JBI.
DR Ensembl; ENSGALG00000009920; Gallus gallus.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR002035; WMF_A.
DR Pfam; PF00815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; WMPADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; WMFA; 2.
KW Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 547 Cochlin.
FT /FTID=PRO_0000020967.
FT DOMAIN 24 117 LCCL.
FT DOMAIN 162 347 WMFA 1.
FT DOMAIN 364 534 WMFA 2.
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
FT DISULFID 30 46 By similarity.
FT DISULFID 50 70 By similarity.
SQ SEQUENCE 547 AA; 59427 MW; 172724242641DF88 CRC64;

Query Match 32.5%; Score 1139; DB 1; Length 547;
Best Local Similarity 37.3%; Pred. No. 1,9e-65;
Matches 229; Conservative 104; Mismatches 165; Indels 116; Gaps 5;

QY 60 VKCPAGQDPRKHYVGTDVVASVSGAAVHSGVLDNKGKILYRKVAGSGVKGYSN 119
DB 44 VLPANCPMLQFVFGDGIYASLSSVCGAALHRTVITNAGAVRVOTLPGENIPAVHAN 103
QY 120 GVQSLSPRMRESFIVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPIPTTA 179
DB 104 GIGQVLSRMASSFSV-----TPGTNN 125
QY 180 QPTVLKOLLAVTAVAPPTTLPRBPSPAATSTSLRPOSVGHRSQEMDLMSTATYSSQN 239
DB 126 ---LALBAVGRSVATARPAT----- 142
QY 240 RPRADPGIQRDPGSAFQKRVGADVSLGLVKEELSTQSLSEPVSLGDPNCKIDSLRID 299
DB 143 -----GKRPKTKLEKKA-----GNKDKKADIAFLID 168
QY 300 GSTIGKRRRIQKQLADVAQAALDIPAGPLMGVQYGDNPATFHNKHTNSRDLKTA 359
DB 169 GSYNIQGRFVLQGNFVKAVAMTLCIGTEGPHVGVVQVASHPKIEFYIKNTAKKEVFA 228
QY 360 IETIRQGLSNVGRASIVTKNFFSKANGRSGAPNVVVVAVDMDPTDKVDEASRLARE 419
DB 229 IKEIGFGGNSNTKALKHAQKFFSMENGRKGIPIIIVFLDGMPSDDLEAGIVARE 288
QY 420 SGNIFFITIGAAENKQYVVERPFAKVCRTNGFSLVQSGFGLHKLQPLVKVVC 479
DB 289 FGVAVFIVYAKPTEELGMVODIGFDKAVCRNNGFSPSYGMPSFGTKYVKPLVQKLC 348
QY 480 DTDRLACSKTCLNADIGFVIDGSSVGTGNFRFVLQFVTNLTYEFEISDTDRIGAVOY 539

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DB 349 SHEOMLCKTYNVNIGFLIDGSSVGESENFRMLMEFISNVAKAFESIDGSKIATVQF 408
QY 540 TYEORLEFGDPKYSKPDILNAIKRVYSGSTGGAINALBQLFPKSKPNRK-LMI 598
DB 409 TYDQRTESFPDYTTKEKVSALNIRKWSGGTIGDLSITTTNNFSPYDGNKQNFV 468
QY 599 LITGRSYDVRIPAMAAHLKGVITVYAGVMAAOEELVATPHARDSEFFVEFDNLH 658
DB 469 ILTDGQSYDDVRGVAVAQKXGIVFSGVAMALDDDKMASERPREHTEFTTEFTGLE 528
QY 659 QYPRRIQNTIFER 672
DB 529 QMVPDVIRGICKDF 542

RESULT 14
COCH_HUMAN STANDARD; PRT; 550 AA.
AC O43405;
DT 30-MAY-2000, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 56.
DE Cochlin precursor (COCH-582).
GN Name=COCH; Synonyms=COCH582; ORFNames=UNQ257/PRO294;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Cochlea;
RX MEDLINE=98110569; PubMed=9441737; DOI=10.1101/geno.1997.5067;
RA Robertson N.G., Skvorak A.B., Yin Y., Weremowicz S., Johnson K.R.,
RA Kovatch K.A., Barette J.F., Bieber F.R., Morton C.C.;
RT "Mapping and characterization of a novel cochlear gene in human and in
RL mouse: a positional candidate gene for a deafness disorder, DFNA9.";
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandelan R.L., Watnabe C., Weand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS ARG-135; ASN-281;
RP SER-353 AND VAL-402.
RA Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahern M.O.,
RA Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
RT "SeattlesNPS, NHLBI HL66682 program for genomic applications, UW-
RT FHRCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [4]
RP N-GLYCOSYLATION, SUBCELLULAR LOCATION, AND PROTEOLYTIC PROCESSING.
RX MEDLINE=22727166; PubMed=12843317; DOI=10.1136/jmg.40.7.479;
RA Robertson N.G., Hamaker S.A., Patriub V., Aster J.C., Morton C.C.;
RT "Subcellular localization, secretion, and post-translational
RT processing of normal cochlin, and of mutants causing the sensorineural
RL deafness and vestibular disorder, DFNA9.";
RN [5]
RP STRUCTURE BY NMR OF 27-126.

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RX MEDLINE=11458442; PubMed=11574446; DOI=10.1093/emboj/20.19.5347;
 RA Leppinsh E., Trexler M., Kaikkonen A., Weigelt J., Banya L.,
 RA Patchy L., Oetting G.,
 RT "NMR structure of the LCCU domain and implications for DFNA9 deafness disorder.";
 RL EMBO J. 20:5347-5353(2001).
 RN [6]
 RN VARIANTS DFNA9 SER-51;
 RP MEDLINE=99021390; PubMed=980555; DOI=10.1078/3118;
 RX Robertson N.G., Lu L., Heller S., Merchant S.N., Bevey R.D.,
 RA Robertson N.G., J., Heller S., Miyamoto R.T., Linticum F.H., Jr.,
 RA McEneaney M., Nadel J.B., Jr., Seldman C.E., Morton C.C., Seldman J.G.,
 RA Neco J.F., Hudspeth A.J.,
 RT "Mutations in a novel cochlear gene cause DFNA9, a human nonsyndromic deafness with vestibular dysfunction.";
 RL Nat. Genet. 20:299-303(1998).
 RN [7]
 RN VARIANT DFNA9 SER-51.
 RP MEDLINE=99135917; PubMed=9931344; DOI=10.1093/hmg/8.2.361;
 RX de Kok Y.J.M., Bom S.J.H., Brunt T.M., Kemperman M.H.,
 RA Franssen E., Verstrucken M., Verhagen W.I.M., Wuyts F.L., Huygen P.L.M.,
 RA D'Haese P., Robertson N.G., Morton C.C., McGuit W.T., Smith R.J.H.,
 RA Declau F., Van de Heyning P.H., Van Camp G.,
 RT "High prevalence of symptoms of Meniere's disease in three families with a mutation in the COCH gene.";
 RL Hum. Mol. Genet. 8:1425-1429(1999).
 RN [9]
 RN VARIANT DFNA9 SER-51.
 RP MEDLINE=99335917; PubMed=10400989; DOI=10.1093/hmg/8.8.1425;
 RX Franssen E., Verstrucken M., Verhagen W.I.M., Wuyts F.L., Huygen P.L.M.,
 RA D'Haese P., Robertson N.G., Morton C.C., McGuit W.T., Smith R.J.H.,
 RA Declau F., Van de Heyning P.H., Van Camp G.,
 RT "High prevalence of symptoms of Meniere's disease in three families with a mutation in the COCH gene.";
 RL Hum. Mol. Genet. 8:1425-1429(1999).
 RN [10]
 RN VARIANT DFNA9 SER-51.
 RP MEDLINE=21193177; PubMed=11295836; DOI=10.1002/humu.37;
 RX Kamaatino M., McGill J., Lynch M., Dahl H.-H.M.,
 RA Kamaatino M., McGill J., Lynch M., Dahl H.-H.M.,
 RT "Identification of a novel COCH mutation, 1109N, highlights the similar clinical features observed in DFNA9 families.";
 RL Hum. Mutat. 17:351-351(2001).
 RN [10]
 RN ERROR.
 RP Kamaatino M., McGill J., Lynch M., Dahl H.-H.M.,
 RA Hum. Mutat. 18:547-548(2001).
 RN [11]
 RN VARIANT DFNA9 SER-119.
 RP MEDLINE=22873884; PubMed=14512963; DOI=10.1038/sj.ejhg.5201043;
 RX Usami S., Takahashi K., Yuge I., Ohtsuka A., Namba A., Abe S.,
 RA Franssen E., Patchy L., Oetting G., Van Camp G.,
 RT "Mutations in the COCH gene are a frequent cause of autosomal dominant progressive cochleo-vestibular dysfunction, but not of Meniere's disease.";
 RL Eur. J. Hum. Genet. 11:744-748(2003).
 RN [12]
 RN CHARACTERIZATION OF VARIANTS DFNA9 SER-51; GLY-66; GLU-88; ASN-109 AND
 RP ARK-117.
 RX MEDLINE=22866966; PubMed=12928864; DOI=10.1007/s00439-003-0992-7;
 RA Grubbs R., Szul T., Sasaki T., Timpl R., Mayne R., Hicks B.,
 RA Szul E.,
 RT "Mutations in COCH that result in non-syndromic autosomal dominant deafness (DFNA9) affect matrix deposition of cochlin.";
 RL Hum. Genet. 113:406-416(2003).
 RN [13]
 RN DISEASE.
 RP MEDLINE=21453839; PubMed=1156867;
 RX DOI=10.1097/00129492-200109000-00009;
 RA Boulaassal M.-R., Tomasi J.-P., Degouy N., Gersdorff M.,
 RT "COCHS2 is a target antigen of anti-inner ear antibodies in autoimmune inner ear disease.";
 RL Otol. Neurotol. 22:614-618(2001).
 CC -1- SUBCELLULAR LOCATION: Secreted protein; extracellular space;

Query Match 32.3%; Score 1129.5; DB 1; Length 550;
 Best Local Similarity 37.1%; Pred. No. 7.8e-65;
 Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

QY 44 INCVKAGKIIDPEFIYKCPAGCCDPKHYHYGTVDYVASYSGAAVHSGVLNDSGGKIL 103
 DB 32 ITCTRGIDIRKEKADVLCPCGCCPLEEFSYVGNITVYASVSSICGAHVHGVINSNGEYVR 91
 QY 104 VRKVGOSGVKGSYNGVOSLSLPRMRESFVLESKPKKGYTPSALTYSSKSPAAOAG 163
 DB 92 VYSLPGRENSSVDANGIOSQMLSRMSASFVTVGK-----SSTQEAATGCA- 137
 QY 164 ETTKAYORPPIPGTTAOPVTLMLAVTVAVATPTLPRSPSASTTSIPRPOSGVHRS 223
 DB 138 -----VSTAHF----- 143
 QY 224 QEMDLWSTATYTSQNNRPADPGIQRDPSGAARQKPVGADVSLGLVKEELSTOSLEPV 283
 DB 144 -----PTGKRLLK-----TPEKK----- 156
 QY 284 SLGDPNCKIDSLFIDGSTSGKRFRIOKQLADVAQALDIGPAGPLMGVVOYGDNPAT 343
 DB 157 -TGKDKCADIAFLIDGSFNIGQRFFNLQKNFVGKVALMLGITEGPHVGLVQASBHPXI 215
 QY 344 HFNKHTNSRDLTALEKITTORGSLSNVGRALSFVTKNPFSSKANGNSGAPNVVVVWD 403
 DB 216 EFLYKNTFSKADVFAIKVEGFRGNSNTGKALKHTKQKFTVDAGVAKGI PKVVVVFID 275
 QY 404 GMPFDKVEASRLAREGINIFFTTIGGAENKQYVEVPNPAKAVCRNTGFSYHVOS 463
 DB 276 GMPSDDIIEAGIVAREGVNFIIVSAKPIPEELGMQDVAFVDFKAVCRNNGFSSYHMPN 335
 QY 464 WFGHAKTLOPLVKVVCOTDLRACSKTCLNSADIGFVIDGSSSVGNGRNTLOFNTLTK 523
 DB 336 WFGTKYKVPVQKLCHEQMMCKCTCYNSVNIAPLIDGSSSVGNSRMLLEFVSNIAK 395
 QY 524 EFEISDTRIGAVOYTYEORLEFGDPKYSKSPDILNAIKRVGYSWGGSTGAALNPALE 583
 DB 396 TFEISDYGAKIAAVOFTYDQRTESFTDYSTKENLAVIRNIRWMSGTATGDAISFTVR 455
 QY 584 QLFK--KSKPNKRLMLITDGRSYDVRIPMAAHLKGVITTYAIGVAAAQEBLEVIAT 641
 DB 456 NVFPGIVDSPPNK-NFLVIVTDGOSYDVQGPAAAHADAGITIFSVGVAMAPLDDLKQWAS 514
 QY 642 HPARDHSFVDEFDNLHQVPRILIONICTEF 672
 DB 515 KPKEASHAFTRFETGLEPIYSDVIRGICRDP 545

RESULT 15
 OSE64_BOVIN PRELIMINARY; PRT; 550 AA.

AC OSE64;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Coagulation factor C homolog, cochlin.
 GN Name=COCH;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Artiodactyla; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Pooleed;
 RX MBLDLINE=2118013; PubMed=11282978; DOI=10.1101/gr.170101;
 RA Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
 RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
 RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-Hickson C.G.,
 RA Petter G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
 RA Keefe J.W.;
 RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA

RT Libraries and construction of a gene index for cattle.";
 RL Genome Res. 11:626-630(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Pooleed;
 RA Hathay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keefe J.W.,
 RA Snelling W.M., Weidmann R.T., Smith T.P.L.;
 RT "Sequencing and analysis of Bos taurus full-length insert cDNA
 RT clones";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC
 CC EMBL: BT020705; AAX08722.1; -, mRNA.
 DR SMR; OSE64; 29-124
 DR Ensembl; ENSBTAG00000021844; Bos taurus.
 DR InterPro; IPR004043; LCCL.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF03815; LCCL; 1.
 DR Pfam; PF00092; VMA; 2.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00603; LCCL; 1.
 DR SMART; SM00327; VMA; 2.
 DR PROSITE; PS50820; LCCL; 1.
 DR PROSITE; PS50234; VWF_A; 2.
 DR SEQUENCE 550 AA; 59594 MW; DB3B21839C68BD209 CRC64;

Query Match 32.1%; Score 1123.5; DB 2; Length 550;
 Best Local Similarity 36.8%; Pred. No. 1.9e-64;
 Matches 232; Conservative 103; Mismatches 177; Indels 119; Gaps 7;

QY 44 INCVKAGKIIDPEFIYKCPAGCCDPKHYHYGTVDYVASYSGAAVHSGVLNDSGGKIL 103
 DB 32 ITCTRGIDIRKEKADVLCPCGCCPLEEFSYVGNITVYASVSSICGAHVHGVINSNGEYVR 91
 QY 104 VRKVGOSGVKGSYNGVOSLSLPRMRESFVLESKPKKGYTPSALTYSSKSPAAOAG 163
 DB 92 VYSLPGRENSSVDANGIOSQMLSRMSASFVTVGK-----SSTQEAATGCA- 137
 QY 164 ETTKAYORPPIPGTTAOPVTLMLAVTVAVATPTLPRSPSASTTSIPRPOSGVHRS 223
 DB 138 -----VSTAHF----- 148
 QY 224 QEMDLWSTATYTSQNNRPADPGIQRDPSGAARQKPVGADVSLGLVKEELSTOSLEPV 283
 DB 149 -----LKTPEKK----- 156
 QY 284 SLGDPNCKIDSLFIDGSTSGKRFRIOKQLADVAQALDIGPAGPLMGVVOYGDNPAT 343
 DB 157 -TGKDKCADIAFLIDGSFNIGQRFFNLQKNFVGKVALMLGITEGPHVGLVQASBHPXI 215
 QY 344 HFNKHTNSRDLTALEKITTORGSLSNVGRALSFVTKNPFSSKANGNSGAPNVVVVWD 403
 DB 216 EFLYKNTFSKADVFAIKVEGFRGNSNTGKALKHTKQKFTVDAGVAKGI PKVVVVFID 275
 QY 404 GMPFDKVEASRLAREGINIFFTTIGGAENKQYVEVPNPAKAVCRNTGFSYHVOS 463
 DB 276 GMPSDDIIEAGIVAREGVNFIIVSAKPIPEELGMQDVAFVDFKAVCRNNGFSSYHMPN 335
 QY 464 WFGHAKTLOPLVKVVCOTDLRACSKTCLNSADIGFVIDGSSSVGNGRNTLOFNTLTK 523
 DB 336 WFGTKYKVPVQKLCHEQMMCKCTCYNSVNIAPLIDGSSSVGNSRMLLKVNSIAK 395
 QY 524 EFEISDTRIGAVOYTYEORLEFGDPKYSKSPDILNAIKRVGYSWGGSTGAALNPALE 583
 DB 396 TFEISDYGAKIAAVOFTYDQRTESFTDYSTKENLAVIRNIRWMSGTATGDAISFTVR 455
 QY 584 QLFK--KSKPNKRLMLITDGRSYDVRIPMAAHLKGVITTYAIGVAAAQEBLEVIAT 641
 DB 456 NVFPGIVDSPPNK-NFLVIVTDGOSYDVQGPAAAHADAGITIFSVGVAMAPLDDLKQWAS 514
 QY 642 HPARDHSFVDEFDNLHQVPRILIONICTEF 672

Db 515 KPESHAFTRREFGTGLEPIVSDVIRGICRDF 545

Search completed: June 7, 2006, 01:19:07
Job time : 307 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 8, 2006, 22:54:30 ; Search time 181 Seconds
(without alignments)
1735.136 Million cell updates/sec

Perfect score: 3502
Sequence: 1 MRFVLTMKASVIEFLVL.....QYVERIIONCTERNQPRN 678

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications_AA_Main:
1: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pcp:*
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6: /EMC_Celestra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|---------------------|-------------------|
| 27 | 3502 | 100.0 | 678 | US-09-997-428-179 | Sequence 179, App |
| 562 | 3502 | 100.0 | 678 | US-10-174-587-150 | Sequence 150, App |
| 626 | 3502 | 100.0 | 678 | US-10-063-742-34 | Sequence 34, Appl |
| 741 | 3502 | 100.0 | 678 | US-10-972-317-34 | Sequence 34, Appl |
| 743 | 3502 | 100.0 | 678 | US-10-950-374-179 | Sequence 179, App |
| 751 | 3502 | 100.0 | 678 | US-11-102-240-34 | Sequence 34, Appl |
| 752 | 3502 | 100.0 | 678 | US-11-103-195-34 | Sequence 34, Appl |
| 753 | 3494.5 | 99.5 | 693 | US-10-408-765A-2507 | Sequence 2507, Ap |
| 754 | 3344 | 95.5 | 656 | US-09-801-736A-2 | Sequence 2, Appli |
| 755 | 1695 | 48.4 | 329 | US-09-732-227-2 | Sequence 2, Appli |
| 756 | 1695 | 48.4 | 329 | US-10-127-101-2 | Sequence 2, Appli |
| 759 | 1129.5 | 32.3 | 550 | US-09-905-291A-227 | Sequence 227, App |
| 1290 | 1129.5 | 32.3 | 550 | US-10-174-587-46 | Sequence 46, Appl |
| 1325 | 1129.5 | 32.3 | 550 | US-10-299-976-227 | Sequence 227, App |
| 1327 | 1129.5 | 32.3 | 550 | US-10-299-937-227 | Sequence 227, App |
| 1337 | 1129.5 | 32.3 | 550 | US-10-298-993-227 | Sequence 227, App |
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1141.265 Million cell updates/sec

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Post-processing: Minimum Match 0%
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and is derived by analysis of the total score distribution.

SUMMARIES

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| 37 | 501.5 | 14.3 | 496 | 1 | US-08-463-180-37 Sequence 37, Appli |
| 38 | 501.5 | 14.3 | 496 | 1 | US-08-001-078A-1 Sequence 1, Appli |
| 39 | 501.5 | 14.3 | 496 | 1 | US-08-897-443-4 Sequence 4, Appli |
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| 43 | 434 | 12.4 | 584 | 2 | US-09-949-016-10340 Sequence 10340, A |
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| 45 | 412 | 11.8 | 1036 | 2 | US-10-104-047-2812 Sequence 2812, App |

ALIGNMENTS

RESULT 1
US-09-991-181-179
Sequence 179, Application US/09991181
Patent No. 6913919
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
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;; PRIOR FILING DATE: 1998-07-07
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RESULT 2

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;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Deenoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman

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;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 678; Conservative 0;

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Db 61 KCPAGCDDPKYHYGVGDVYASYSVCGAAVHSGVLDNSGCKILVRKAGSGYKGSYNG 120
QY 121 VQSLSPRMRESFVLVESKPKKGVTPSALTYSSSSPAQAQETTAYOYRPIPGTTAQ 180
Db 121 VQSLSPRMRESFVLVESKPKKGVTPSALTYSSSSPAQAQETTAYOYRPIPGTTAQ 180
QY 181 PVTLMQLLATVVAATPTTLPRPSPASATTSIPRPOSVGHRQEMDLWSTATYSSQNR 240
Db 181 PVTLMQLLATVVAATPTTLPRPSPASATTSIPRPOSVGHRQEMDLWSTATYSSQNR 240
QY 241 PRADPGIORODPSGAARQKVGADVSLGLVPKSELSTQSLPEVSLDPNCKIDLSFLIDG 300
Db 241 PRADPGIORODPSGAARQKVGADVSLGLVPKSELSTQSLPEVSLDPNCKIDLSFLIDG 300
QY 301 STSIGKRFRIOKQLADVAQALDIGPAGPLMGVVOGDNPATFNLKHTNSRDLKTAI 360
Db 301 STSIGKRFRIOKQLADVAQALDIGPAGPLMGVVOGDNPATFNLKHTNSRDLKTAI 360

QY 361 EKTORGCLSNVGRALISFVTKNFFSKANGNSGANNVWVWDGWPDTKVEBASRLAES 420
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QY 421 GINIFFTIEGAENKQYVVEPNANKAVCTTNGFYSLHVOSWGLKHTLOPLVKRVC 480
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QY 481 TDRLACSKTCNSADIGFVIOGSSVSGTGNPFTVQFVNTLKEKEISDTPRIGAVOYT 540
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QY 541 YEORLEFGFDKXSSKPDILNMIKRVGYWSGCTSTGAINFALBQLFKSKPKMKRLMTLI 600
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QY 601 TDGRSYDDVRIPAMAHLKGVITTAIGVMAAQELEVIAHPADHSEFVDEPNLHOY 660
Db 601 TDGRSYDDVRIPAMAHLKGVITTAIGVMAAQELEVIAHPADHSEFVDEPNLHOY 660
QY 661 VPRIIQNTCTEFSNOSP RN 678
Db 661 VPRIIQNTCTEFSNOSP RN 678

RESULT 3
US-09-997-333-179
Sequence 179, Application US/09997333
Patent No. 6953836
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Roy, Margaret Ann
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C27
CURRENT APPLICATION NUMBER: US/09/997,333
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 KCPAGCDDPKYHYGTDVYASVSSVCGAAVHSGVLDNSGGKILVRKYAGSGYKGSYNG 120
QY 121 VQSLPRMRESFVLSEKPKGVTYPSALTSSSSPAAOAGETTKAYORPPIGTTAQ 180
Db 121 VQSLPRMRESFVLSEKPKGVTYPSALTSSSSPAAOAGETTKAYORPPIGTTAQ 180
QY 181 PVTLMQLAATVAVATPTTLPRPSPASSTSIIPRPOVGHRSQEMDLWSTATYSSQNR 240
Db 181 PVTLMQLAATVAVATPTTLPRPSPASSTSIIPRPOVGHRSQEMDLWSTATYSSQNR 240
QY 241 PRADPGIQRDDPSGAARQKVGADVSLGLVPKELSTQSLPEPVSIGPNCKIDSLFIDG 300
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Db 361 EKITQRGSLNVGSAISFVTKNFFSKANGRSAPNVVVVVDGPTDKVEASRLARES 420
QY 421 GINIFFTTIGGAENEQYVVERPFANKAVCRNNGFSLHVSQWFGHAKTLOPLVKRVC 480
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QY 661 VPRIONICTEPNSQPN 678
Db 661 VPRIONICTEPNSQPN 678

RESULT 4
US-09-992-598-179
Sequence 179, Application US/09992598
Patent No. 6956108
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 3502; DB 2; Length 678;
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DB 121 VQSLSPRMRRESFVLESKEPKGVTPSALTYSKSPAAOAGETTRAYORPPIGTTAQ 180
QY 181 PVLMLQLLAVTVAVATPTTLPRPSPSAATSTSIIPQSVGHRSGEMDLMTATYTSSQNR 240
DB 181 PVLMLQLLAVTVAVATPTTLPRPSPSAATSTSIIPQSVGHRSGEMDLMTATYTSSQNR 240
QY 241 PRADPGIQRDDPSGAAGFQKVGADVSLGLVKEELSTOSLEPVSLGDPNCKIDISFLIDG 300
DB 241 PRADPGIQRDDPSGAAGFQKVGADVSLGLVKEELSTOSLEPVSLGDPNCKIDISFLIDG 300
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DB 421 GINIFFITIEGAENKQYVTEPNPANKAVERTNGFSLHYQSFGLKTLQPLVKRYCD 480
QY 481 TDRLACSKTCNLSADIGFVIDGSSVGTGNRTVLOPFVTNLTKRFEISDTPTRIGAVOYT 540
DB 481 TDRLACSKTCNLSADIGFVIDGSSVGTGNRTVLOPFVTNLTKRFEISDTPTRIGAVOYT 540
QY 541 YEORLEFGFDKYSKSPDILNAIKRQVYWSGGTSTGAAINFALDQLPKSKXPKRKLMI 600
DB 541 YEORLEFGFDKYSKSPDILNAIKRQVYWSGGTSTGAAINFALDQLPKSKXPKRKLMI 600
QY 601 TDGRSYDDVRIPMAAHLKGVITTAIGVAAAQOELEVIATHPARDHSFVDEPDNLHOY 660
DB 601 TDGRSYDDVRIPMAAHLKGVITTAIGVAAAQOELEVIATHPARDHSFVDEPDNLHOY 660
QY 661 VPRITONICTEFPNSOPRN 678
DB 661 VPRITONICTEFPNSOPRN 678
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RESULT 5
US-09-989-735-179
; Sequence 179, Application us/09989735
; Patent No. 6972185
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, Paul J.
; APPLICANT: Gutney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 3502; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 KCPAGCCDPKYHVVGTDVYASYSVCGAAVHSGVLNDNGGKILVRKVAQSGYKGSYNG 120
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QY      121 VQSLPFRRESFVLSESKPKKGYTPPALTYSSSKSPAQAQETTKAYORPPIPGTTAQ 180
DB      121 VQSLPFRRESFVLSESKPKKGYTPPALTYSSSKSPAQAQETTKAYORPPIPGTTAQ 180
QY      181 PVTLMQLLAVTVAVATPTTLTPRPSAASSTISIPRPSVGHRSQEMDMSTATTYSSQNR 240
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DB      301 STSIGKRFRIOQLADVAQALDIPGAPLMGVVQYGDNPATHTNLTHTNSRDLKTAI 360
QY      361 EKIQRGGLSVGRLAISVTNKFPSKANGNSGAPNVVVVAVDGPPTTKVEASRLARES 420
DB      361 EKIQRGGLSVGRLAISVTNKFPSKANGNSGAPNVVVVAVDGPPTTKVEASRLARES 420
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DB      481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVYLQFVTNLTKFEISDTDTTRIGAVQYT 540
QY      541 YEOGLEFGFDKYSKSPDILNAIKRVGYWSSGTSGAINFALBOLFKSKSKNKKMLILI 600
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QY      601 TDGSRSDVDVPIPMAAAHLKGVITAYAGVMAAOELEVIAIHPARDHSFFVDEEDNLHOY 660
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QY      661 VPRIONICTEFPNSQPRN 678
DB      661 VPRIONICTEFPNSQPRN 678

RESULT 6
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; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C60
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 VQSLSPRMRESFVLESKPKKGVTPSALTYSSSKSPAAGETTKAYQRPPIPGTTAQ 180
DB 121 VQSLSPRMRESFVLESKPKKGVTPSALTYSSSKSPAAGETTKAYQRPPIPGTTAQ 180
QY 181 PVTLMQLLAVTVAVATPTTLPPRSPAASTTSIPRQSVGHRQEMDLNSTATYSSQNR 240
DB 181 PVTLMQLLAVTVAVATPTTLPPRSPAASTTSIPRQSVGHRQEMDLNSTATYSSQNR 240
QY 241 PRADPGIORODPSGAFAQKPVGADVSLGVPKBELSTOSLEPVSIGDPNCKTIDLSPLIDG 300
DB 241 PRADPGIORODPSGAFAQKPVGADVSLGVPKBELSTOSLEPVSIGDPNCKTIDLSPLIDG 300
QY 301 STSIGRRPRIOXOLLADYVQALDIDGPAELMGVVOYGNPATHEMLKTHNSRDLKTAI 360
DB 301 STSIGRRPRIOXOLLADYVQALDIDGPAELMGVVOYGNPATHEMLKTHNSRDLKTAI 360

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Qy 481 TDRLACKSKCLNSADIGFPIIDGSSSVGTGNFRTVLOFTNLTKEFISDTRIGAVOYT 540
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Qy 541 YEQRLPEFGDKYSKPDILNATKRVGVMGSGTGAATNFALFOLFKSKPNKRMKMLI 600
Db 541 YEQRLPEFGDKYSKPDILNATKRVGVMGSGTGAATNFALFOLFKSKPNKRMKMLI 600
Qy 601 TDGRSYDDVRIPAMAHLKGVITTYAIGVAMAAQEELEVIATHPARDHSFVDEFDNLHOY 660
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Qy 661 VPRITQNTCTERNSQPRN 678
Db 661 VPRITQNTCTERNSQPRN 678

RESULT 7

US-09-997-514-179

Sequence 179, Application US/09997514

Patent No. 7019116

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botsstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C6
CURRENT FILING DATE: US/09/997,514
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25

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PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MNTVLTMKASYIEHVLVLTGVSNKETAIRKPKPTVQINCDVAKIIDPEFV 60
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61 KCPAGCOPKHYVGTDVYASYSVCGAAVHSGVLNDSGKILVKKVAGOSGYKSYNSG 120
121 VQSLSPRWRESFVLESKPKKGVTPSALTYSSSKSPAQAQGETTKAYORPPIGTTAQ 180
121 VQSLSPRWRESFVLESKPKKGVTPSALTYSSSKSPAQAQGETTKAYORPPIGTTAQ 180
181 PVTLMQLAVYVAVATPTTLPRSPSAATTSIIPRPOSVGRHSQMDLWSTATYSSQNR 240
181 PVTLMQLAVYVAVATPTTLPRSPSAATTSIIPRPOSVGRHSQMDLWSTATYSSQNR 240
241 PRADPGIORODPSGAFOKPVGADVSLGVPEELSTSLBVSIGDPNCKIDLSFLIDG 300
241 PRADPGIORODPSGAFOKPVGADVSLGVPEELSTSLBVSIGDPNCKIDLSFLIDG 300
301 STSISGRRRRIQKOLLADVAQALDIGAPGLMGVVQYGDNPATHTNLTHTNSRDLKTAI 360
301 STSISGRRRRIQKOLLADVAQALDIGAPGLMGVVQYGDNPATHTNLTHTNSRDLKTAI 360
361 EKITORGCLSNVGRALISFTKNFESKANCNRGANNVVMVMDGMPDIVEREASRLARS 420
361 EKITORGCLSNVGRALISFTKNFESKANCNRGANNVVMVMDGMPDIVEREASRLARS 420
421 GINIFPITTEGAANEKQYVVEPNFANKAVCTNGFYSLHVOSWEGHLHTLOPLVGRVCD 480
421 GINIFPITTEGAANEKQYVVEPNFANKAVCTNGFYSLHVOSWEGHLHTLOPLVGRVCD 480
481 TDRLACSKTCLNSADIGFVIDSSSVGTGNFRTVLQFVTNLTKREIISDTDRIGAVQYT 540
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541 YEOBLEFGDKYSSKPDILNAIKRQVYWGSGTGAATFALQULFKSKKPKMKLMIIL 600
541 YEOBLEFGDKYSSKPDILNAIKRQVYWGSGTGAATFALQULFKSKKPKMKLMIIL 600
601 TGRSYDVDRIPAMAAHLKGVITTYAIGVMAAOELEVATAPADHSFVDFDNLHXY 660
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661 VRIIIONICTEFNSOPRN 678
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RESULT 8
US-09-989-728-179
Sequence 179, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C72
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLTMRASVLEMFVLVLTGVSHNKETAKKIKPKFTVPQINC DVAKGIIDPEFIY 60
DB 1 MTRVLTMRASVLEMFVLVLTGVSHNKETAKKIKPKFTVPQINC DVAKGIIDPEFIY 60

QY 61 KCPAGCQDPRKYHYGTDVYASYSVCGAAHSGVLNDSGKILVRKXAGSGYKGSYNG 120
DB 61 KCPAGCQDPRKYHYGTDVYASYSVCGAAHSGVLNDSGKILVRKXAGSGYKGSYNG 120

QY 121 VOSLSLPRMRESVIVESKPKGVTPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
DB 121 VOSLSLPRMRESVIVESKPKGVTPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180

QY 181 PVTLMQLLAVTVAVATPTTLPRSPSAASTTSPRQSVGHRSGQMDLWSTATYTSQNR 240
DB 181 PVTLMQLLAVTVAVATPTTLPRSPSAASTTSPRQSVGHRSGQMDLWSTATYTSQNR 240

QY 241 PRADPGIQRQDPSGGAARQKRVGADVSLGPKKELSQSLSEPIVSLGDPNCKIDSLFIDG 300
DB 241 PRADPGIQRQDPSGGAARQKRVGADVSLGPKKELSQSLSEPIVSLGDPNCKIDSLFIDG 300

QY 301 STSIGRRFRIGQLADVAQALDIGPAGPLMGVVGYNPATFHLKTHNSRDLKTAI 360

DB 301 STSIGRRFRIGQLADVAQALDIGPAGPLMGVVGYNPATFHLKTHNSRDLKTAI 360
QY 361 EKITRGGLSNVGRASISFTKNFESKANGNRGAPNWWWVDGMPDTEVEASRLAES 420
DB 361 EKITRGGLSNVGRASISFTKNFESKANGNRGAPNWWWVDGMPDTEVEASRLAES 420

QY 421 GINIFPITTEGAENKQYVEPNFANKAVCTNGTFYSIAVOSWFLGKHTLOPLVRYVCD 480
DB 421 GINIFPITTEGAENKQYVEPNFANKAVCTNGTFYSIAVOSWFLGKHTLOPLVRYVCD 480

QY 481 TDLRACSKTCLNSADIGFYIDGSSVGTGNFTYVQFTNLTKEBEISDTDRIGAVQYT 540
DB 481 TDLRACSKTCLNSADIGFYIDGSSVGTGNFTYVQFTNLTKEBEISDTDRIGAVQYT 540

QY 541 YEOBLEFGFDKXSSPDILNAIKRVYSGSTGAALFALEOLFKSKPNKRKLMI 600
DB 541 YEOBLEFGFDKXSSPDILNAIKRVYSGSTGAALFALEOLFKSKPNKRKLMI 600

QY 601 TGRSYDVRIRPAMAAHLKGVITTYAIGVMAAQEELVATHPARDHSFVDFDNLHOY 660
DB 601 TGRSYDVRIRPAMAAHLKGVITTYAIGVMAAQEELVATHPARDHSFVDFDNLHOY 660

QY 661 VPRIIQICTEFNSQPRN 678
DB 661 VPRIIQICTEFNSQPRN 678

RESULT 9
US-09-997-349-179
Sequence 179, Application US/09997349
Patent No. 7034106
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Beststein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C37
CURRENT APPLICATION NUMBER: US/09/997,349
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945

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| 2 | PRIOR FILING DATE: 1998-06-17 |
| 3 | PRIOR APPLICATION NUMBER: 60/0895999 |
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| 5 | PRIOR APPLICATION NUMBER: 60/0896000 |
| 6 | PRIOR FILING DATE: 1998-06-17 |
| 7 | PRIOR APPLICATION NUMBER: 60/0896533 |
| 8 | PRIOR FILING DATE: 1998-06-17 |
| 9 | PRIOR APPLICATION NUMBER: 60/0898001 |
| 10 | PRIOR FILING DATE: 1998-06-18 |
| 11 | PRIOR APPLICATION NUMBER: 60/0899070 |
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| 13 | PRIOR APPLICATION NUMBER: 60/0899088 |
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| 15 | PRIOR APPLICATION NUMBER: 60/0899477 |
| 16 | PRIOR FILING DATE: 1998-06-19 |
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| 18 | PRIOR FILING DATE: 1998-06-19 |
| 19 | PRIOR APPLICATION NUMBER: 60/0899522 |
| 20 | PRIOR FILING DATE: 1998-06-19 |
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| 26 | PRIOR FILING DATE: 1998-06-22 |
| 27 | PRIOR APPLICATION NUMBER: 60/0903449 |
| 28 | PRIOR FILING DATE: 1998-06-23 |
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| 30 | PRIOR FILING DATE: 1998-06-23 |
| 31 | PRIOR APPLICATION NUMBER: 60/0904229 |
| 32 | PRIOR FILING DATE: 1998-06-24 |
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| 36 | PRIOR FILING DATE: 1998-06-24 |
| 37 | PRIOR APPLICATION NUMBER: 60/0904444 |
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| 40 | PRIOR FILING DATE: 1998-06-24 |
| 41 | PRIOR APPLICATION NUMBER: 60/0904722 |
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| 60 | PRIOR FILING DATE: 1998-06-26 |
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| 64 | PRIOR FILING DATE: 1998-07-01 |
| 65 | PRIOR APPLICATION NUMBER: 60/0914788 |
| 66 | PRIOR FILING DATE: 1998-07-02 |
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 3502; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MRYVLTWKASVIEFVLVLTGHSNKEATKIKRPFTVPOINCVDYKAGKIIDPEIV 60
Db      1  MRYVLTWKASVIEFVLVLTGHSNKEATKIKRPFTVPOINCVDYKAGKIIDPEIV 60

Qy      61  KCPAGCCOPKHYVCTDVYASVSCGAHVSGVLDNCGGKILVRKVAQSGYKSYNG 120
Db      61  KCPAGCCOPKHYVCTDVYASVSCGAHVSGVLDNCGGKILVRKVAQSGYKSYNG 120

Qy      121  VQSLPWRRESFVLESKPKKGVTPALTYSSSKSPAQAQGETTKAYORPPIGTTAQ 180
Db      121  VQSLPWRRESFVLESKPKKGVTPALTYSSSKSPAQAQGETTKAYORPPIGTTAQ 180

Qy      181  PVTLMQLIAVTVAVATPTTLPRPSPSAATSTISIPRQSGVHRSQEMDLSTATYSSQNR 240
Db      181  PVTLMQLIAVTVAVATPTTLPRPSPSAATSTISIPRQSGVHRSQEMDLSTATYSSQNR 240

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Db      241  PRADGICOROPBSGAFOKPVGADVSLGIVPEELSTOSLEPVSIGDPNCKIDLSFLIDG 300

Qy      301  STSICKRRFRIOKOLADVAAQALDIPAGPLMGVVQYGDNPATHTFNLTHTNSRDLKTAI 360
Db      301  STSICKRRFRIOKOLADVAAQALDIPAGPLMGVVQYGDNPATHTFNLTHTNSRDLKTAI 360

Qy      361  EKITORGGISNVGRAISFVTKNFESKANGNRSGANVVVVMYDGNPTDKVEBASRLAES 420
Db      361  EKITORGGISNVGRAISFVTKNFESKANGNRSGANVVVVMYDGNPTDKVEBASRLAES 420

Qy      421  GINIFITIEGAENEKQVVEPNPANKAVCTNGFYSLHVOSWGLHKTLOPLVKRYVD 480
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Qy      661  VPRITONICTEFNSOPRN 678
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RESULT 10
US-09-997-653-179
; Sequence 179, Application US/0997653
; Patent No. 7034132
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Deenoeyers, Luc
; APPLICANT: Ealon, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerder, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PLC38
; CURRENT APPLICATION NUMBER: US/09/997, 653
; CURRENT FILING DATE: 2001-11-15
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 3; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MRYVVLTKASVTEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVAKGIIDEEFIY 60
 QY 61 KCPAGCDDPKYHYVGDVAVSYSSVCGAAVHSGVLNCGKILVRVAGSGYKGSYSNG 120
 DB 61 KCPAGCDDPKYHYVGDVAVSYSSVCGAAVHSGVLNCGKILVRVAGSGYKGSYSNG 120
 QY 121 VQSLSLPRWRESFIVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPIPGTTAQ 180
 DB 121 VQSLSLPRWRESFIVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPIPGTTAQ 180
 QY 181 PVTLMQLLAVTVAVATPTTLPSPSPAASSTSIIPRQSVGHRSGQEMDLWSTATYTSQNR 240
 DB 181 PVTLMQLLAVTVAVATPTTLPSPSPAASSTSIIPRQSVGHRSGQEMDLWSTATYTSQNR 240
 QY 241 PRADPGIORODPSGAFFQKPVGVADVSLGLVPEKELSTQSLPEVSLDPPNCKIDLSFLIDG 300
 DB 241 PRADPGIORODPSGAFFQKPVGVADVSLGLVPEKELSTQSLPEVSLDPPNCKIDLSFLIDG 300

QY 301 STSICKRRFRIOKOLADVAQALDIGPAGPLMGVVQYGDNPATHTFNLTHTNSRDLKTAI 360
Db 301 STSICKRRFRIOKOLADVAQALDIGPAGPLMGVVQYGDNPATHTFNLTHTNSRDLKTAI 360
QY 361 EKITRGGLSNVGRALISFTKNPFPSKANKNRSGAPVVVVVMDGNPTDVEASRLAARS 420
Db 361 EKITRGGLSNVGRALISFTKNPFPSKANKNRSGAPVVVVVMDGNPTDVEASRLAARS 420
QY 421 GINIFPITIEGAENEKOYVVEPNFANKAVCRITNGFYSLSHVOSFGLHNTLQPLVRYVD 480
Db 421 GINIFPITIEGAENEKOYVVEPNFANKAVCRITNGFYSLSHVOSFGLHNTLQPLVRYVD 480
QY 481 TDRLACSKTCLNSADIGFVIDSSVGTGNFRTVLQFVTNLTKFEISDTRIGAVOYT 540
Db 481 TDRLACSKTCLNSADIGFVIDSSVGTGNFRTVLQFVTNLTKFEISDTRIGAVOYT 540
QY 541 YEORLEFDFDKSSKRPDLINAIKRVYWSGGTSGAINFALQPLKSKPKRKLMLI 600
Db 541 YEORLEFDFDKSSKRPDLINAIKRVYWSGGTSGAINFALQPLKSKPKRKLMLI 600
QY 601 TDGRSYDVRIPAMAHLKGVITTYAIGVAMAOEELVYATHPADHSFVDEPNLHOY 660
Db 601 TDGRSYDVRIPAMAHLKGVITTYAIGVAMAOEELVYATHPADHSFVDEPNLHOY 660
QY 661 VPRIIONICTEFNSOPRN 678
Db 661 VPRIIONICTEFNSOPRN 678

RESULT 11
US-09-989-293A-179
Sequence 179, Application US/09989293A

Patent No. 7034136
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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DB 1 MRTVLTMKASVIMFVLVLTGVHSNKEFTAKKIKRPFVTPQINCVCYKAGKITDPEFIV 60
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DB 61 KCPAGCDDPKYHYVGTGVVSVSGAAVHSGVLDSGGKILVRKYAGSGYKGSYNG 120
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DB 121 VQSLSPRMRESFVLBSKPKKGYTPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
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DB 181 PVTLMOLLAVTVAVATPTTLPRPSPAASTTSIRPQSVGHRSEMDLMTATYTSSQNR 240
QY 241 PRADPGIORODPSGAOKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDSLFLIDG 300
DB 241 PRADPGIORODPSGAOKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDSLFLIDG 300
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DB 301 STSIGKRFRIOQLLDVAQALDIGPAGPLMGVVOYGDNPATFNLKTHNSRDLKTAI 360
QY 361 EKITORGGLSNVGAISFTYTNKFSKANGNRSGAPNVVVWDMFDDKVEBARLRES 420
DB 361 EKITORGGLSNVGAISFTYTNKFSKANGNRSGAPNVVVWDMFDDKVEBARLRES 420
QY 421 GINIFITIEGAANEQYVVEPNFANKAVCRTGFSLSHVQSPFGLHKTLOPLVKRVC 480
DB 421 GINIFITIEGAANEQYVVEPNFANKAVCRTGFSLSHVQSPFGLHKTLOPLVKRVC 480
QY 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFVTNLTKFEISDTRIGAVQYT 540
DB 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOFVTNLTKFEISDTRIGAVQYT 540
QY 541 YEORLEFGFDYSSKRPDIINAIRKVGWSGTSGAALINFALBOLFCKSKPNKRMIL 600
DB 541 YEORLEFGFDYSSKRPDIINAIRKVGWSGTSGAALINFALBOLFCKSKPNKRMIL 600
QY 601 TDGRSYDDVRIPAAAHILKGVITYAIGVANAQEELEVIATHPARDHSFVDEEDNLHOY 660
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DB 661 VPRIIIONICTEFNSQPRN 678

RESULT 12
US-09-907-794A-227
Sequence 227, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi


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1  APPLICANT: Botstein, David
2  APPLICANT: Deenoyers, Luc
3  APPLICANT: Bacon, Dan L.
4  APPLICANT: Ferrara, Napoleone
5  APPLICANT: Filvaroff, Ellen
6  APPLICANT: Fong, Sherman
7  APPLICANT: Gao, Wei-Qiang
8  APPLICANT: Gerber, Hanspeter
9  APPLICANT: Gertsen, Mary E.
10 APPLICANT: Goddard, A.
11 APPLICANT: Godowski, Paul J.
12 APPLICANT: Grimaldi, Christopher J.
13 APPLICANT: Gurney, Austin L.
14 APPLICANT: Hillan, Kenneth, J.
15 APPLICANT: Kljavin, Ivar J.
16 APPLICANT: Mather, Jennie P.
17 APPLICANT: Pan, James
18 APPLICANT: Paoni, Nicholas F.
19 APPLICANT: Roy, Margaret Ann
20 APPLICANT: Stewart, Timothy A.
21 APPLICANT: Tumas, Daniel
22 APPLICANT: Williams, P. Mickey
23 APPLICANT: Wood, William, I.
24 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
25 FILE REFERENCE: 10466-14
26 CURRENT APPLICATION NUMBER: US/09/907,794A
27 PRIOR FILING DATE: 2001-07-17
28 PRIOR APPLICATION NUMBER: PCT/US00/04414
29 PRIOR FILING DATE: 2000-02-22
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52 PRIOR APPLICATION NUMBER: PCT/US99/28565
53 PRIOR FILING DATE: 1999-12-02
54 PRIOR APPLICATION NUMBER: PCT/US99/30095
55 PRIOR FILING DATE: 1999-12-16
56 PRIOR APPLICATION NUMBER: PCT/US99/30911
57 PRIOR FILING DATE: 1999-12-20
58 PRIOR APPLICATION NUMBER: PCT/US99/30999
59 PRIOR FILING DATE: 1999-12-20
60 PRIOR APPLICATION NUMBER: PCT/US00/00219
61 NUMBER OF SEQ ID NOS: 423
62 SEQ ID NO 227
63 LENGTH: 550
64 TYPE: PRT
65 ORGANISM: Homo sapiens
66 US-09-907-794A-227

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| Query Match | 32.3%; | Score 1129.5; | DB 2; | Length 550; |
| Best Local Similarity | 37.1%; | Pred. No. 9.5e-97; | | |
| Matches 234; | Conservative 103; | Mismatches 175; | Indels 119; | Gaps 7; |

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Db 32 ITCFRRGLDIRREKKAQDVLCPGCGCPREEFSVGNINIVASVSSIGCAVHVGVINSQGPVR 91
QY 104 VAKVAGOSGYSKASVANGVQSLSLPRWRESFVILESPKPKGVTPYPSALTYSSSKSPAQAQ 163
Db 92 VYSLRGRENVSVSDANQIGOSQMLSRMSASFYTKGK-----SSTQBATGQA- 137
QY 164 ETTKAYQRPPIGTTAQPVTMLQOLAVYAVATPTTLPRPSPBASTTSIPRPQOSVGRS 223
Db 138 -----VSTHAP----- 143
QY 224 QEMDLMSTATYTSQGNRPAPDPCIQRDPSGAFOKPGVADVSLGLVPKEELSTQSLPEV 283
Db 144 -----PTGKRLKK-----TPEKK----- 156
QY 284 SLGDPNCKIDLSFLIDGSTSIGKRFRPRLQKOLLADVAQALDIPAGPLNGVQYQDNPAT 343
Db 157 -TGNMDCADIAFLIDGSFNIGQRFRNLOKNFVGKALMLGIGTBEPHYGLVQASHPKI 215
QY 344 HENLKTHTNSRDLKTAIEKITQRGGLSNVGRALSEVTKNPFSGKANGNSGAPNVVVMVD 403
Db 216 EBYLKNFTSIAKQVLPALIKVSGFRGSGNSGKALKHTAQKFFTVDAVVRKGI PKVWVFID 275
QY 404 GHPPTKVEBASLARESGNIFITITEGAANEKQVYVBNPANKAVCTGTNGSYSLHYOS 463
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QY 464 WFLGKHTLOPLVKRVCDDTRRLACSKTCLNSADIGFVIDSSSVGTGNFRFTVLOFTNLTK 523
Db 336 WFGTTKYKPELVQKCTHEGQMGCSKITCVNSVIAFLIDSSSVGDBNFFLMLFEVSNIAK 355
QY 524 EEISDTRIGAVQYTYEQRLFEFGDKYSSKPDILINAIKRVGWSGTSYGAINPALE 583
Db 396 TEISIDIGAKLIAVQFTYDQRTFESTDYSTKENYLAIVIRINRWSGATGDAISFTVR 455
QY 584 QLFK--KSKPNRKMLILTDTRSVDVRIIPMAAHLKGVITYIYALGVANAQAQEELEVIAT 611
Db 456 NVFGPIRESPNK-NFLVITVTDQSYDDVQGPAAAHADAGITTFISGVAVAPLDDLKDMS 514
QY 642 HPARDHSFVDFEDNMLHQVPRITONICTEF 672
Db 515 KPESHAFPTREFTGLEPIVSDVITGICRDF 545

RESULT 13
US-09-905-125A--227
/ Sequence 227, Application US/09905125A
/ Patent No. 6664376
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Geider, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tunas, Daniel

```

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: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/905,125A
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20584
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/21547
: PRIOR FILING DATE: 1999-09-15
: PRIOR APPLICATION NUMBER: PCT/US99/23089
: PRIOR FILING DATE: 1999-10-05
: PRIOR APPLICATION NUMBER: PCT/US99/28214
: PRIOR FILING DATE: 1999-11-29
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: 1999-11-30
: PRIOR APPLICATION NUMBER: PCT/US99/28564
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/28565
: PRIOR FILING DATE: 1999-12-02
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: 1999-12-16
: PRIOR APPLICATION NUMBER: PCT/US99/30911
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US99/30999
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: PCT/US00/00219
: PRIOR FILING DATE: 2000-01-05
: NUMBER OF SEQ ID NOS: 423
: SEQ ID NO 227
: LENGTH: 550
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-905-125A-227

Query Match      32.3%; Score 1129.5; DB 2; Length 550;
Best Local Similarity 37.1%; Pred. No. 9.5e-97;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

QY 44 INCVAKGKIIDPEFIYKCPAGCDDPKHVVGTVDVYASVSCGAAYHSGVLNDSGKIL 103
DB 32 ITCTRGADIRKEKADADVLCPEGCPLEESVYGNIVYASVSSICGAAYHGVISNGGEVR 91
QY 104 VRKAGCGSYGKSYNGVQSLSLPRMRESFVLESKPKGVYTSALTYSSSKSPAQAQ 163
DB 92 VYSLPGKENTSSVANGQSGMLSRMSASFVTKG-----SSTQEAATGA- 137
QY 164 ETKKAYRPPPIPGTTAOPVTLMQLAAVTVAATPTTLPRSPSAASTSTIRPOSVGHRS 223
DB 138 -----VSTAHF----- 143
QY 224 QEMDLWSTATYTSQNRPRADPGIORODPSGAHFOKPYGADVSLGVLPKEELSTOSLEPV 283
DB 144 -----PTGKRLLK-----TPKKF----- 156
QY 284 SLGDPNCKIDLSFLIDSTSGKRRFRIOQLADVAQALDIDGPAFLMGVQYGDNPAT 343
DB 157 -TGKDKCKADIAFLIDGSFNIGCRFRNLQKNFVGKVALMLGIGREGPHVGLVQASEHKI 215
QY 344 HFNLTHTNSBDLKTALIEKLTORGGLSNVGAISFVTNKNFSSKANGNKGAPNVVVVMD 403
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DB 216 EFLYKNFTSADVDYFAAKEVGFRRGNSNTGKALKHTAQKEFTVDAGVRKGI PKVVVFID 275
QY 404 GMPDXYEBSRLARESGINIFFTIEGALENEKQYVEPFAKAVACRTNGFSLVQS 463
DB 276 GMPSDDIEEAGIVAREGVNVFVSVAKPTPEELGMVQDVTYVDKAVCRNNGFFSYMPN 335
QY 464 WFGIAKTLQPLVKVRCUDBRLACSKTCLNSADIGFVIDSGSSVGTGNFRVLOFTNLTK 523
DB 336 WFGTTKTVKPLVQGLCTHQBQMSKCTCYNVNIATFLIDGSSVGDNSNFRILMEFVSNIAK 395
QY 524 EPEISDPTDRIGAVQYTYEQRLPEFGPKYSKPIILAIKRVGYSGCTSTGAINFAL 583
DB 396 TFEISDGIKIAAQQFYDQRTFESSFYDSTKENVLAVINIRIYWSGCTATGDAISFTVR 455
QY 584 QLFK--KSKPKRKLMLITDGRSDYDVRIPAMAHLKGVITYAIGVAMAAQEELEYIAT 641
DB 456 NVFGPIRESFNK-NFLVITVDGQSYDDVQGPAAAHAGITIRFSVGVAAPLDLKMAS 514
QY 642 HPARDHSFVDEFDNLHQYVPRIIQNICTEF 672
DB 515 KPKESHAFFTRFETGLEPIVSDVIRGICRDF 545

RESULT 14
US-09-902-775A-227
: Sequence 227, Application US/09902775A
: Patent No. 6686451
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc.
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Bolstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Batson, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvarolef, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Hillan, Kenneth, J.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Mather, Jennie P.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William, I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: 10466-14
: CURRENT APPLICATION NUMBER: US/09/902,775A
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: 2000-02-22
: PRIOR APPLICATION NUMBER: US 60/143,048
: PRIOR FILING DATE: 1999-07-07
: PRIOR APPLICATION NUMBER: US 60/145,698
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: US 60/146,222
: PRIOR FILING DATE: 1999-07-28
: PRIOR APPLICATION NUMBER: PCT/US99/20594
: PRIOR FILING DATE: 1999-09-08
: PRIOR APPLICATION NUMBER: PCT/US99/20944
: PRIOR FILING DATE: 1999-09-13
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 227
LENGTH: 550
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-227

Query Match 32.3%; Score 1129.5; DB 2; Length 550;

Best Local Similarity 37.1%; Pred. No. 9.5e-97;

Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

44 INCVKAKGKIDPEITVCPAGCOPKHYVVDYVYSSVCGAAVHSGVLNDSGGKIL 103
32 ITCTRGADIKKADVLCPGCPEEBSVGNIVYASVSTCGAAVRGVINSGGFVR 91
104 VRKVGSGYKGSYNGVQSLPRMRESFVLESKPKGVYPSALTYSSSKSPAQAG 163
92 VYSLPGRENTSSVDANGIQSGMLSRWSASFVYTKGK-----SSTQEAETGA- 137
164 ETTAKVQRPPIPTTAQEVITLMQLAVYVAATPTTLRPSBSAATSTIRPQSVGRS 223
138 -----VSTAH----- 143
224 QEMLMSTATYTSSQNRPRADPGIORDPGSAFPQGVADVSLGVKEELSTQSLBPV 283
144 -----PTGKRKK-----TPEKK----- 156
284 SLGDPNCKIDSLFLIDGSTSIGKRFRIOKOLLADVAQALDIGPAGPLMGVQXGNPAT 343
157 -TGKKDCADIAFLIDGSFNIGORFNLQKNFVKVALLMIGTSGPHVGLVQASHEHKI 215
344 HENLKTHNSDCLKTAIEKITQRGSLSVGRALSFVTYNFSSKANGNSGAPNVVYVWD 403
216 EFLYKNFTSADQVFAIKEVGFGRGNSNTGKALKTAQKFFVDAGVAKGIPIKVVVVID 275
404 GMPDKVEEARLARESGINFFLITIEGAENKGVYVEPNPANKAVYORTGFSYLAHQ 463
276 GMPSDDIIEAGIVAREFVNPFIVSAKPIBELAMVDVTFVDVACRKNNGFFSYHPN 335
464 WFGAHTLOPLVKKVCDTRDLACSKTCLNSADIGFVIDSSSVGTGNFRVLPQVNTLTK 523
336 WFGTKYVVKPLVQKLCHEGMMCKSTCYNSVNIAPLIDGSSSVGBSNRLMLEFNSLAK 395
524 EFEISDTRIGAVOYTYEORLERGFQYSSKPDILNAIKAVGWSSGSGTGAALNPALE 583
396 TFEISDIGAKIAAOFYTDORTEFSTYSTEENLAVIRNIRYMSGGTAAGDAISFTVR 455
584 QLPK--KSKPKRKLMLITDGRSYDVIRIPAMAAHLGVTYATGVMAAQEELVAT 641
456 NVFGPIRSPPK-NFLVITDQSYDDVQGPAAAHADGITTFSGVAMAPLDLKDMS 514
642 HPARDHSEFVDEFDNLHQVPRIIQNICTEF 672

Db 515 KPESHAFTRFPTGLEPIVSDVIRIGICRDP 545
RESULT 15
US-09-906-700-227
Sequence 227, Application US/09906700
Patent No. 6723535
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eacon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Par, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US/09/906,700
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-700-227

Query Match 32.3%; Score 1129.5; DB 2; Length 550;
Best Local Similarity 37.1%; Pred. No. 9.5e-97;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

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OY 44 INCVYKAKKIIDPEFIYKCPAGCCDPKHYVYGTVDYASYSVCNAVHSGVLDNSGGKIL 103
Db 32 ITCFTRGIDIRKEKADVLCPGGCCPLEEFSYGNIVYASVSSICGAHVHGVISNSGPFVR 91
OY 104 VRKVGOSGYSYNGVQSLSLPRMRESFVLESGPKKGVTYPSALTYSSSKSPAAQAG 163
Db 92 VYSLPGRENSSVDANGIQSOMLSHMSASFVTYKKG-----SSTQENTGQA- 137
OY 164 ETRKAYORPPIPGTTAOPVTLMOLLAVTVAVATPTTLPRPSPSASTTSIPRQSVGHR 223
Db 138 -----VSTAHF----- 143
OY 224 QEMDMNSTATYTSQNRPRADPGIORQDPSGAAFQKPYGADVSLGLVPKEELSTOSLEPV 283
Db 144 -----PTGKRLLK-----TPKK----- 156
OY 284 SLGDPNCKIDSLPIDGSTSGKRRFRIOQLADVAQALDGPAGPLMGVVOYGDNPAT 343
Db 157 -TGKDCADKADIAFLIDGSFNIGORRPNQKPFVGKVALMLGITEGPHVGLVQASEHPXI 215
OY 344 HFNILKTHNSRDLTAIEKITORGGLSNVGRASIFVTNPFSSKANGNSGAPNVVYVMD 403
Db 216 EFLYLNFTSADVLFAIKEVGFRRGNSNTGKALKHTAQKFTVDAGVRKGIPIKVYVVFID 275
OY 404 GMPFDKVEBSRLAREGINIFFTIEGAENEEKYVVERPANKAVCRTNGEYSLHQS 463
Db 276 GMPSDDIEEAGIVAREGVNFIIVSAKPIPEELGMVODVTFVDAVCRNNGFFSYHMPN 335
OY 464 WFGAHTLQPLVYKRVCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRVLOEVTNLT 523
Db 336 WFGTTKYVPLVQKLTCHQCMCKTCYNSVNIAPFLIDGSSSVGDSNFRMLLEFVSNIAK 395
OY 524 EFEISDTRIGAVQYTYEQRLEFGPKYSKPDILNAIKRVGYSGGTSTGAINEPALE 583
Db 396 TFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAIVIRNIARYMSGTATGDAISFTVR 455
OY 584 QLEK--KSKPNKRLMLITDGRSYDDYRIPAMAHLKGVTYTAIGVWMAAOBELEVIAT 641
Db 456 NVFGPIRESPNK-NFLVIVTDGQSDYDVGPAALAAHDGITTFVGVAMAPLDLDKDMAS 514
OY 642 HPARDHSFVDFDNLHQYVPRITONICTEF 672
Db 515 KPKEASHAFTRFTGLEPIVSDVIRGICRDF 545
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Search completed: June 7, 2006, 01:20:53
Job time : 55 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 7, 2006, 01:14:17 ; Search time 44 Seconds

(without alignments)
1482.613 Million cell updates/sec

Title: US-10-063-540-34

Sequence: 1 MRLTVLTKASVIEMLPLV.....QYVPRITQICTEFNSQPRN 678

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR.80:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 554 | 15.8 | 3124 | 2 A40020 | collagen alpha 1(X |
| 2 | 504.5 | 14.4 | 3137 | 2 A37797 | collagen alpha 3(V |
| 3 | 501.5 | 14.3 | 496 | 2 A37979 | cartilage matrix p |
| 4 | 490 | 14.0 | 493 | 2 A33809 | cartilage matrix p |
| 5 | 490 | 14.0 | 500 | 2 S65222 | cartilage matrix p |
| 6 | 471.5 | 13.5 | 3176 | 2 CGH03A | collagen alpha 3(V |
| 7 | 331 | 9.5 | 1857 | 2 S31212 | collagen alpha 1(X |
| 8 | 331 | 9.5 | 1888 | 2 S78476 | collagen alpha 1(X |
| 9 | 329.5 | 9.4 | 1747 | 2 A54849 | collagen alpha 1(V |
| 10 | 329.5 | 9.4 | 1747 | 2 A45974 | collagen alpha 1(X |
| 11 | 314.5 | 9.0 | 567 | 2 T28797 | hypothetical prote |
| 12 | 298 | 8.5 | 741 | 2 T46488 | hypothetical prote |
| 13 | 280.5 | 8.0 | 929 | 2 S15037 | type XII collagen |
| 14 | 279 | 8.0 | 3051 | 2 S42373 | hypothetical prote |
| 15 | 266 | 7.6 | 2813 | 1 VMU | hypothetical prote |
| 16 | 262.5 | 7.5 | 843 | 1 A40970 | undulin 1 - human |
| 17 | 252.5 | 7.2 | 1019 | 1 A32856 | collagen alpha 1(V |
| 18 | 231 | 6.6 | 1153 | 1 RWH0UB | cell surface glyco |
| 19 | 229 | 6.5 | 550 | 2 T23760 | hypothetical prote |
| 20 | 229 | 6.5 | 1153 | 2 S00551 | leukocyte surface |
| 21 | 228 | 6.5 | 1163 | 1 RWH0UC | cell surface glyco |
| 22 | 226.5 | 6.5 | 427 | 2 G00039 | von Willebrand fac |
| 23 | 226.5 | 6.5 | 1025 | 2 S34839 | collagen alpha 1(V |
| 24 | 213.5 | 6.1 | 414 | 2 S50323 | von Willebrand fac |
| 25 | 213.5 | 6.1 | 1286 | 2 T18397 | protein MO1E10.2 I |
| 26 | 210.5 | 6.0 | 2098 | 2 T18397 | protein CTRP - mal |
| 27 | 209.5 | 6.0 | 1022 | 2 S04111 | collagen alpha 2(V |
| 28 | 209 | 6.0 | 918 | 2 S23377 | collagen alpha 2(V |
| 29 | 205 | 5.9 | 1028 | 1 CGH03A | collagen alpha 1(V |

| | | | | | |
|----|-------|-----|-------|----------|--------------------|
| 30 | 205 | 5.9 | 1029 | 1 S21369 | collagen alpha 2(V |
| 31 | 204 | 5.8 | 11055 | 2 T16580 | hypothetical prote |
| 32 | 203.5 | 5.8 | 1170 | 2 S03308 | cell surface glyco |
| 33 | 203.5 | 5.8 | 1180 | 2 A35854 | integrin alpha-1 c |
| 34 | 200 | 5.7 | 238 | 2 C35243 | collagen alpha 2(V |
| 35 | 200 | 5.7 | 917 | 2 S09646 | collagen alpha 2(V |
| 36 | 200 | 5.7 | 1018 | 1 CGH02A | collagen alpha 2(V |
| 37 | 195 | 5.6 | 1163 | 2 I56126 | lymphocyte fuction |
| 38 | 193 | 5.5 | 1151 | 2 A45226 | integrin alpha-1 c |
| 39 | 188.5 | 5.4 | 272 | 2 A55348 | integrin alpha 1 - |
| 40 | 187.5 | 5.4 | 1170 | 2 T45914 | integrin alpha 2 s |
| 41 | 184.5 | 5.3 | 643 | 2 T19549 | hypothetical prote |
| 42 | 184.5 | 5.2 | 1181 | 2 A33958 | integrin alpha-2 c |
| 43 | 178 | 5.1 | 763 | 2 I50807 | complement factor |
| 44 | 171 | 4.9 | 712 | 2 A45638 | immunodominant mic |
| 45 | 170.5 | 4.9 | 1178 | 2 S44142 | VLA-2 protein homo |

ALIGNMENTS

RESULT 1
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collagen alpha 1(XII) chain precursor - chicken
M:Alternate names: fibrochimerin
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C:Accession: A40020, A34485, B34485, A28037, S23814, S2254, S28811
R:Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shimomura, T.; Tanaka, H.; Nishida, Y.; Obar
J. Cell Biol. 115, 209-221, 1991
A:Title: The complete primary structure of type XII collagen shows a chimeric molecule w
nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.
A:Reference number: A40020; MUID:92011862; PMID:1918137
A:Accession: A40020
A:Molecule type: mRNA
A:Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>
A:Cross-references: UNIPARC:UPI0000171233; EMBL:J05137; NID:9211284; PIDN:AAA48635.1; PI
A:Accession: B34485
A:Molecule type: protein
A:Residues: 2772-2792; 2846-2873 <GOR2>
A:Cross-references: UNIPARC:UPI0000173C3F; UNIPARC:UPI0000173C40
R:Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A:Title: Type XII collagen: A large multidomain molecule with partial homology to type I
A:Reference number: A34485; MUID:90062079; PMID:2584192
A:Accession: A34485
A:Molecule type: mRNA
A:Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>
A:Cross-references: UNIPARC:UPI0000171233; EMBL:J05137; NID:9211284; PIDN:AAA48635.1; PI
A:Accession: B34485
A:Molecule type: protein
A:Residues: 2772-2792; 2846-2873 <GOR2>
A:Cross-references: UNIPARC:UPI0000173C3F; UNIPARC:UPI0000173C40
R:Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987
A:Title: Type XII collagen: A large multidomain molecule with partial homology to type I
A:Reference number: A28037; MUID:87311590; PMID:3476925
A:Accession: A28037
A:Molecule type: mRNA
A:Residues: 2960-2976, 'F', 2978-3074, 'AG', <GOR3>
A:Cross-references: UNIPARC:UPI0000171234; EMBL:M17375; NID:9211649; PIDN:AAA48718.1; PI
A:Note: this sequence has been revised in reference A34485
R:Koch, M.; Bernasconi, C.; Chiquet, M.
Eur. J. Biochem. 207, 847-856, 1992
A:Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of
A:Reference number: S23814; MUID:92362621; PMID:1333460
A:Accession: S23814
A:Molecule type: protein
A:Residues: 'X', 1333, 'Q', 1335-1347, 1914-1928, 2504, 'X', 2506, 'X', 2508-2511, 'X', 2513-2517 <
A:Cross-references: UNIPARC:UPI0000173C41; UNIPARC:UPI0000173C42; UNIPARC:UPI0000173C43
R:Dublet, B.; van der Rest, M.
J. Biol. Chem. 267, 17724-17727, 1992
A:Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-
A:Reference number: S22254; MUID:88087065; PMID:3121603
A:Accession: S22254
A:Molecule type: protein

A:Residues: 2883-2832, 'T', 2834, 'R', 2836-2843, 3002-3014 <DNB>
A:Cross-references: UNIPARC:UPI0000173C44, UNIPARC:UPI0000173C45
R:Title: B.
Biochim. Biophys. Acta 1171, 97-98, 1992
A:Title: The two splice variants of collagen XII share a common 5' end.
A:Reference number: S28811, MUID:93042014, PMID:1420368
A:Accession: S28811
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-24, 1189-1257, 'S', 1259-1263, 'E', 1265-1280 <TRU>
A:Cross-references: UNIPARC:UPI0000173C46, EMBL:X67327
C:Genetics:
A:Introns: 2845/3, 2863/3, 2887/3, 2899/3, 2922/1, 2985/1, 3008/1, 3065/1
C:Keywords: alternative splicing; cell binding; coiled coll; connective tissue; disulfide
F:1-23/Domains: signal sequence #status predicted <SIG>
F:24-314/Product: collagen alpha 1(XII) chain #status predicted <MAT>
F:24-1189-3124/Product: collagen alpha 1(XII) chain short splice form #status predicted
F:24-114/Domains: IIIA #status predicted <IIIA>
F:24-105/Domains: fibronectin type III repeat homology <FN3A>
F:137-301/Domains: von Willebrand factor type A repeat homology <VWA1>
F:332-425/Domains: IIIB #status predicted <IIIB>
F:332-414/Domains: fibronectin type III repeat homology <FN3B>
F:437-601/Domains: von Willebrand factor type A repeat homology <VWA2>
F:629-1178/Domains: IIIC #status predicted <IIIC>
F:630-711/Domains: fibronectin type III repeat homology <FN3C>
F:721-802/Domains: fibronectin type III repeat homology <FN3D>
F:812-895/Domains: fibronectin type III repeat homology <FN3E>
F:905-986/Domains: fibronectin type III repeat homology <FN3F>
F:995-1076/Domains: fibronectin type III repeat homology <FN3G>
F:1086-1169/Domains: fibronectin type III repeat homology <FN3H>
F:1197-1361/Domains: von Willebrand factor type A repeat homology <VWA3>
F:1384-1465/Domains: IIID #status predicted <IIID>
F:1474-1557/Domains: fibronectin type III repeat homology <FN3I>
F:1474-1557/Domains: fibronectin type III repeat homology <FN3J>
F:1566-1647/Domains: fibronectin type III repeat homology <FN3K>
F:1655-1738/Domains: fibronectin type III repeat homology <FN3L>
F:1756-1838/Domains: fibronectin type III repeat homology <FN3M>
F:1847-1928/Domains: fibronectin type III repeat homology <FN3N>
F:1937-2019/Domains: fibronectin type III repeat homology <FN3O>
F:2028-2110/Domains: fibronectin type III repeat homology <FN3P>
F:2119-2199/Domains: fibronectin type III repeat homology <FN3Q>
F:2207-2294/Domains: fibronectin type III repeat homology <FN3R>
F:2335-2490/Domains: von Willebrand factor type A repeat homology <VWA4>
F:2438-2440/Region: cell adhesion #status predicted
F:2509-2750/Domains: IXP, homologous to NC4 domain of type IX collagen #status predicted
F:2751-2902/Domains: collagenous COL2 #status predicted <COL2>
F:2889-2901/Region: cell attachment (R-G-D) motif
F:2903-2945/Domains: non-collagenous NC2 #status predicted <NC2>
F:2946-3048/Domains: collagenous COL1 #status predicted <COL1>
F:3049-3124/Domains: non-collagenous NC1 #status predicted <NC1>
F:321, 1006, 1032, 1044, 1512, 1767, 2210, 2273, 2532, 2683/binding site: carbohydrate (Asn) (coverage
F:2780, 2789, 2836, 2842, 2860, 2866, 2869, 3004, 3007/modified site: hydroxyproline (Pro) #stat

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Oy 451 CERNGF-----YSLHVSQSMFGI-----467
Db 356 STSQITGRVQCIIPMIAGKQHVLSVGPQTALTANVDSLPTREYQIVNVAMKGLTPESEPI 415
Oy 468 ---HKTLPVYKRVCDTDRCLACSKTCLNSADIGFVIDGSSSVGTGNFRVLTQPVNTLTKE 524
Db 416 TIMEKTQGVK-----QVECSRGVDVAKADVFLVDGSSYSIGIANFVKRAPELEVAVKS 468
Oy 525 FEISTDTRICAVQTYTEERLEFPGDPKYSKSPDILNAIKRVGWSGTSNGAINFALQ 584
Db 469 FEISPRKQVQISLVQYSRDPHEFSLNRKRVKDIQALITPEFGSGTNGKMTYVREK 528
Oy 585 LF---KKSQPNRKSMILITIDRSYDDVRIIPMAALKGVITYAGVMAAOELEVIAT 641
Db 529 VFVTSKSGRPVPRVWMLITIDGSSDAFKEPPIKLRADADVEIRAVGVKDAVRTELEAIAS 588
Oy 642 HPARDHSFFVDEFDNLHQYVPRIIQNTCTEFSNQ 675
Db 589 PPAEFHVTVTEEDPDAFORISFELTQSVCLRIEQE 622

RESULT 2
A37797
collagen alpha 3(VI) chain precursor - chicken
C|Species: Gallus gallus (chicken)
C|Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext_change 16-Aug-2004
C|Accession: A37797; A34270; A32674
R|Doliana, R.; Bonaldo, P.; Colombatti, A.
J. Cell Biol. 111, 2197-2205, 1990
A|Title: Multiple forms of chicken alpha3(VI) collagen chain generated by alternative splicing
A|Reference number: A37797; MUID:91035630; PMID:197751
A|Accession: A37797
A|Molecule type: mRNA
A|Residues: 1-253;312-321;434-453;504-518;635-655;704-717;832-853 <DOL>
A|Cross-references: UNIPROT:P15989; UNIPARC:UPI0000173C31; UNIPARC:UPI0000173C32; UNIPARC:UPI0000173C33
R|Bonaldo, P.; Russo, V.; Buccicotti, F.; Doliana, R.; Colombatti, A.
Biochemistry 29, 1245-1254, 1990
A|Title: Structural and functional features of the alpha3 chain indicate a bridging role
A|Reference number: A34270; MUID:90212613; PMID:2322559
A|Accession: A34270
A|Molecule type: mRNA
A|Residues: 224-2871 <BON>
A|Cross-references: UNIPARC:UPI0000173C38; GB:M24282
A|Note: The authors translated the codon TTC for residue 1916 as Leu and TTC for residue
R|Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 264, 20235-20239, 1989
A|Title: The carboxyl termini of the chicken alpha3 chain of collagen VI is a unique motif
A|Reference number: A32674; MUID:90062147; PMID:2584214
A|Accession: A32674
A|Molecule type: mRNA
A|Residues: 2151-2159;2792-3137 <BO2>
A|Cross-references: UNIPARC:UPI0000173C39; UNIPARC:UPI0000173C3A; GB:M24282
C|Genetics: 30/1; 236/1; 437/1; 638/1; 838/1
A|Introns: 30/1; 236/1; 437/1; 638/1; 838/1
C|Superfamily: collagen VI
C|Keywords: alternative splicing; cell binding; coiled coil; connective tissue; extracellular matrix
F|1-25/Domain: signal sequence #status predicted <SIG>
F|26-3137/Product: collagen alpha 3(VI) chain #status predicted <MAT>
F|26-3042/Domain: non-collagenous #status predicted <NMC>
F|36-202/Domain: von Willebrand factor type A repeat homology <W01>
F|239-404/Domain: von Willebrand factor type A repeat homology <W02>
F|442-607/Domain: von Willebrand factor type A repeat homology <W03>
F|642-807/Domain: von Willebrand factor type A repeat homology <W04>
F|840-1004/Domain: von Willebrand factor type A repeat homology <W05>
F|1033-1197/Domain: von Willebrand factor type A repeat homology <W06>
F|1237-1400/Domain: von Willebrand factor type A repeat homology <W07>
F|1439-1604/Domain: von Willebrand factor type A repeat homology <W08>
F|1639-1804/Domain: von Willebrand factor type A repeat homology <W09>
F|1838-2010/Domain: von Willebrand factor type A repeat homology <W10>
F|2043-2378/Domain: collagenous #status predicted <COL>
F|2045-2047/Region: cell attachment (R-G-D) motif
F|2153-2155/Region: cell attachment (R-G-D) motif

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F:2159-2161/Region: cell attachment (R-G-D) motif
 F:2379-3137/Domain: non-collagenous #status predicted <CNC-
 F:2405-2577/Domain: von Willebrand factor type A repeat homology <W11>
 F:2623-2806/Domain: von Willebrand factor type A repeat homology <W12>
 F:2863-2846/Domain: platelet glycoprotein Ib-like #status predicted <GPI>
 F:2954-3039/Domain: fibronectin type III repeat homology <FN3>
 F:3072-3122/Domain: animal knittiz-type proteinase inhibitor homology <BPI>
 F:201,2084,2436,2563,2581,2663,2867,2920,3003/Binding site: carbohydrate (asn) (covalent

[illegible]


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Qy 293 D$PFI0$ST$IGKR$R$P$IO$Q$OLLADV$A$O$LDIG$B$P$LM$GV$Q$D$P$ATH$P$N$K$TH$N 352
Db 39 DLVFI$T$SS$VR$P$OE$F$K$V$F$U$S$R$V$IE$G$LD$V$G$N$STR$G$V$IN$A$S$V$K$O$F$S$K$TH$Q 98
Qy 353 SRD$K$T$A$E$K$T$T$O$R$G$L$SN$V$R$A$IS$F$V$T$K$N$F$F$S$K$AN$R$S$G$AP$N$--VVVV$V$D$G$M$P$D$K 409
Db 99 KAE$LL$O$A$V$O$R$IE$P$T$G$T$M$T$G$I$O$F$A$IS$R$A$F$S$D$T$E$G$A$R$L$R$S$P$N$INK$V$AI$V$T$D$G$R$P$D$G 158
Qy 410 VEE$A$R$L$A$R$E$G$IN$F$F$I$-----TIE$A$E$N$E$K$O$Y$Y$E$R$P$A$K$--AV 450
Db 159 VQD$V$A$R$A$R$O$G$IE$F$A$IG$V$R$V$D$M$H$T$L$R$O$A$S$E$P$LD$D$H$V$Y$V$E$S$Y$I$E$K$T$H$N$P$D$E$A$F 218
Qy 451 C-----RTNG$F$Y$S$L$H$V$O$S$M$F$G$H$K$T$O$E$P$V$K$R$C$D$T$R$L$A$C$S$K$T$C$IN 492
Db 219 CV$S$D$L$C$A$T$G$D$H$D$E$Q$O$IC$IST$P$G$S$Y$K$C$K$G$F$T$I$M$N$D$----G$K$T$C$S$----A$C$S$G$S$G$S 269
Qy 493 S$A$D$I$G$E$V$I$D$G$S$S$V$G$T$N$F$R$V$LO$F$V$T$N$L$T$Y$E$F$E$I$S$D$T$R$I$G$A$V$O$Y$T$E$Q$R$L$E$F$G$D$K 552
Db 270 A$L$D$V$F$L$ID$G$S$K$Y$P$E$N$F$E$V$K$K$F$IN$Q$I$V$E$S$L$E$V$E$K$O$A$V$G$L$V$O$Y$S$S$V$R$O$E$P$L$O$Q 329
Qy 553 S$K$D$P$I$N$A$IR$V$G$W$S$G$T$G$A$IN$F$A$L$E$O$L$F$--K$K$S$P$N$K$R$K$M$ILL$T$D$P$R$S$Y$D$V 609
Db 330 N$K$K$D$I$K$A$V$K$K$M$A$M$E$K$T$M$G$A$K$Y$L$V$O$S$F$E$I$A$N$G$A$R$G$V$P$K$V$I$V$T$D$G$S$O$Y$I 389
Qy 610 R$I$P$A$A$H$L$K$V$IT$Y$A$IV$A$M$A$O$E$E$V$I$A$T$H$P$A$R$D$S$F$V$E$D$E$D$N$H$O$V$P$R$I$O$N$C 669
Db 390 T$D$A$K$K$A$D$O$L$P$R$M$F$A$V$G$N$A$V$E$D$E$L$R$E$I$A$S$E$P$A$B$H$Y$F$T$A$D$P$R$T$S$N$IG$K$L$O$M$K$IC 449
Qy 670 TE 671
Db 450 VE 451

```

RESULT 5

060322
cartilage matrix protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S66522
R/Ascoli, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hirtl, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996
A>Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein c
A/Reference number: S66522; MUID:96270751; PMID:8665920
A/Accession: S66522
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-500 <AS>
A/Cross-references: UNIPROT:P51942; UNIPARC:UP10000029480; EMBL:U53035; NID:g1163178; P
C/Genetics:
A/Gene: CMP
C/Superfamily: cartilage matrix protein; EGF homology; von Willebrand factor type A repe
F.1-29/Domain: signal sequence #status predicted <SIG>
F.30-500/Product: cartilage matrix protein #status predicted <MAT>
F.43-210/Domain: von Willebrand factor type A repeat homology <WMA1>
F.231-266/Domain: EGF homology <EGF>
F.277-441/Domain: von Willebrand factor type A repeat homology <WMA2>

Query Match **14.0%:** Score 490; DB 2; Length 500;
Best Local Similarity **28.8%:** Pred. No.5.3e-25;
Matches 130; Conservative 72; Mismatches 184; Indels 66; Gaps 8;

Qy 266 SLGLVPEKEELSTOSLEPVSLDPPNCKIDLSFLDGISTIGRRRIQKOLLADVAOALDI 325
 ||| |:: :: ||| :|::|
Db 27 SLSLVIPQRGHLCRTRP-----DLVEVVDSRSRVREVEEKVKVFLLSQYIESLDV 77

Qy 326 GPAPPLNGVOYGDNPATHEFNLKTHTNSRDILKTAIEKITRGGLSNVGRAISPYTKNOFFS 385
 :||: |:| :|: |::| :|:|:
Db 78 GPNATRGVLNVYSTAVKREFPLPAHGSVASIILOVRRIQPSTGTMTGIALQLQAFITAKLS 137

Qy 386 KANNRSGAAP---VVVMVDGWCPDKUYEASRLAREGINIIFLTTEGAANE--KOY 440
 ::: :::|:| :|:| :|:|:
Db 138 DAEGGRARSPISKVIIVTDTGRPODSVRVDSEBARAAGIELFAIGL-GRYDAKTLNQIA 196

[illegible]

RESULT 6

collagen alpha 3 (VI) chain precursor [validated] - human
N/Contains: collagen alpha 3 (VI) chain, splice form A5/N10(-)
C/Species: Homo sapiens (man)
C/Date: 21-Nov-1993 #sequence revision 12-Nov-1999 #ext: change 16-Aug-2004
A/Ccession: A59140; S13679; S24465; A57083; S28776; S00245; C31952; C29848; S26510; S48-
R.Chu, M.L.
submitted to GenBank, May 1998
A/Reference number: A59140
A/Ccession: A59140
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-3176 <CH>
A/Cross-references: UNIPROT:P12111; UNIPARC:UPI0000126DAF; GB:X52023; NID:G3127925; P1DN:
R.Chu, M.L.; Zhang, R.Z.; Pan, T.; Stokes, D.; Conway, D.; Kuo, H.T.; Glanville, R.; Mayne,
EMBO J. 9, 385-393, 1990
A/Title: Mosaic structure of globular domains in the human type VI collagen alpha-3 chain
A/Reference number: S13679; MUID:90151612; PMID:1689238
A/Ccession: S13679
A/Molecule type: mRNA
A/Residues: 1-30,237-313, 'CWN', 318-322, 'AR', 326-385, 'FD', 1818-1819, 'ID', 1822-3176 <CH>
A/Cross-references: UNIPARC:UPI0000173C14; EMBL:X52022; NID:G3127925
A/Ccession: S24465
A/Molecule type: protein
A/Residues: 574-585;965-973, 'X', 975-976;1306-1325;1361-1377;1381-1401;1473-1506, 'X', 1508-
1962, 'X', 1964-1965;2018-2037;2374-2410;2445-2459;2466-2469, 'X', 2471-2474;2504-2508, 'X',
A/Cross-references: UNIPARC:UPI0000173C15; UNIPARC:UPI0000173C16; UNIPARC:UPI0000173C17;
CIC; UNIPARC:UPI0000173C1D; UNIPARC:UPI0000173C26; UNIPARC:UPI0000173C1E; UNIPARC:UPI0000173C1F;
10000173C25; UNIPARC:UPI0000173C26; UNIPARC:UPI0000173C27
R.Zanusser, S.; Dollana, R.; Segat, D.; Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 267, 24082-24089, 1992
A/Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain
A/Reference number: S28776; MUID:93054780; PMID:1339440
A/Ccession: A57083
A/Molecule type: DNA
A/Residues: 310-328 <ZAN>
A/Cross-references: UNIPARC:UPI0000173C28
A/Ccession: S28776
A/Molecule type: mRNA
A/Residues: 32-126, 'AK', 129-136, 'L', 138-236 <ZA>
A/Cross-references: UNIPARC:UPI0000173C28; GB:S49432; NID:G260296; P1DN:AB24261.1; P1D:
R.Chu, M.L.; Mann, K.; Deutzmann, R.; Pribula-Conway, D.; Hen-Chen, C.C.; Bernard, M.P.;
Eur. J. Biochem. 168, 309-317, 1987
A/Title: Characterization of three constituent chains of collagen type VI by peptide sequ
A/Reference number: S00126; MUID:88029444; PMID:365927
A/Ccession: S00245
A/Molecule type: mRNA; protein
A/Residues: 2024-2046;2092-2156, 'R', 2203-2208, 'X', 2210-2211, 'X', 2213-2227;2228-2251;2314-
A/Cross-references: UNIPARC:UPI000016A705; UNIPARC:UPI0000173C29; UNIPARC:UPI0000173C2A;
ID:G3135034

F:442-525/Domain: fibronectin type III repeat homology <FN3C>
 F:534-614/Domain: fibronectin type III repeat homology <FN3D>
 F:623-707/Domain: fibronectin type III repeat homology <FN3B>
 F:741-823/Domain: fibronectin type III repeat homology <FN3F>
 F:832-914/Domain: fibronectin type III repeat homology <FN3G>
 F:922-1009/Domain: fibronectin type III repeat homology <FN3H>
 F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 9.5%; Score 311; DB 2; Length 1857;
 Best Local Similarity 24.8%; Pred. No. 1,76-13;
 Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

174 IGTGAQVTLMLQALVAVAPPTLPRSPSAASTSTIRPQSVGRSQEMD----- 227
 Db 713 IGVTTALPTT-----VTTTTTATTPKPTIAVFR-----GVRNLVIDDETTSS 757
 Qy 228 ---LMSATATYSSQNR-----PRADPGIORODPSGAAPKPVGAADVSLGVPKELS 276
 Db 758 LRVVWDISDHAQOFRTYTLTAKGDRAEALMPGRQNTLLQ-----LLPDTREYK 809
 Qy 277 TQSL-----EPVSLGDPNCKIDLSFLIDGSTSGRRFRIOKOLADVQAALDIPGAP 330
 Db 810 VTIPIYADGCVSAAGKTLPLS-----APRNLRVSDWYNRLRISWD-APRSP 859
 Qy 331 LMG--VVOYQDN---PATFNLKHTNSRDLKTAIEKTORGGLSNVGRASIVTKNFFS 385
 Db 860 TMGRIRIVKSIINVGPA---LETFVGD-DINTIL-----ILNLFSGTEYSVKVPAS 906
 Qy 386 KANG---NRSGAPNVVVWVGWPTDKVEASRLAR---ESGINIFETIEGAENEMKQY 439
 Db 907 YSTGFSDALGVAKTLVGLVNTLDYQVRMTSLCAQOLRHATATVAVIESLVGKKQ- 965
 Qy 440 VVEBNFANKAVCRTNGYSL--HVQSWFGLHKTLO----- 472
 Db 966 --EVNLGG-GVPR-HCFEELMPGTEYKISVHAQOEIEGPAVSIMETTLPPPTQPTSPS 1021
 Qy 473 -----PLVKRYCDTRLACSKTCLNSADIGVIDSSVGNFRVTLQFVTNLTKE 524
 Db 1022 TTLPPPTIPPAKEVCKAAK-----ADLVFLVDSMSIGDDNFNKIISFLYSTVGA 1071
 Qy 525 FE-ISDITRIGAVQYTYEORLEFGFDKYSKPDILNAIKRVGYWSGTSGAALNFAL 583
 Db 1072 LDKTGPDTQVAIIQFSDDPRTFELNAYKTKETLLEAIQIAYKGGNTGKAIKHARE 1131
 Qy 584 QLF-----KSKRNKRKMLITLDGSRSDVAVIPAMAHLKGVITVAIGVAMAQOELE 637
 Db 1132 VLFPGAGMKRGKIP---KVLVVIITDGSQDDVKNVSRMQLDGFSPFALGVADADYSELV 1188
 Qy 638 VIATHPARDSFFVDFEDNHLQVPRRIQNIC 669
 Db 1189 NIGSKPSEBHVFFVDDPDAFTKIEDLITFVC 1220

RESULT 8

collagen alpha 1(XIV) chain precursor, long form - chicken

C/Species: Gallus gallus (chicken)

C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004

C/Accession: S78476; S31211

R/Tueb, B.

submitted to the EMBL Data Library, January 1993

A/Reference number: S78476

A/Accession: S78476

A/Molecule type: mRNA

A/Residues: 1-1888 <TRU>

A/Cross-references: UNIPROT:P32018; UNIPARC:UPI0000126D31; EMBL:X70793; NID:G288872; PTC

R/Weichl, C.; Tueb, J.; Kessler, B.; Winterhalter, K.H.; Tueb, B.

Eur. J. Biochem. 212, 483-490, 1993

A/Title: Complete primary structure of chicken collagen XIV.

A/Reference number: S31211; MUID:93185668; PMID:844186

A/Accession: S31211

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-416;1460-1811,1843-1888 <WAE>
 A/Cross-references: UNIPARC:UPI00001773F4; UNIPARC:UPI00001773F5; EMBL:X70793
 C/Genetics:
 A/Gene: Coll14A1
 C/Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:129-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
 F:156-330/Domain: fibronectin type III repeat homology <FN3A>
 F:325-433/Domain: von Willebrand factor type A repeat homology <VWA1>
 F:442-525/Domain: fibronectin type III repeat homology <FN3B>
 F:534-614/Domain: fibronectin type III repeat homology <FN3C>
 F:623-707/Domain: fibronectin type III repeat homology <FN3D>
 F:741-823/Domain: fibronectin type III repeat homology <FN3F>
 F:832-914/Domain: fibronectin type III repeat homology <FN3G>
 F:922-1009/Domain: fibronectin type III repeat homology <FN3H>
 F:1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 9.5%; Score 311; DB 2; Length 1888;
 Best Local Similarity 24.8%; Pred. No. 1,76-13;
 Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

174 IGTGAQVTLMLQALVAVAPPTLPRSPSAASTSTIRPQSVGRSQEMD----- 227
 Db 713 IGVTTALPTT-----VTTTTTATTPKPTIAVFR-----GVRNLVIDDETTSS 757
 Qy 228 ---LMSATATYSSQNR-----PRADPGIORODPSGAAPKPVGAADVSLGVPKELS 276
 Db 758 LRVVWDISDHAQOFRTYTLTAKGDRAEALMPGRQNTLLQ-----LLPDTREYK 809
 Qy 277 TQSL-----EPVSLGDPNCKIDLSFLIDGSTSGRRFRIOKOLADVQAALDIPGAP 330
 Db 810 VTIPIYADGCVSAAGKTLPLS-----APRNLRVSDWYNRLRISWD-APRSP 859
 Qy 331 LMG--VVOYQDN---PATFNLKHTNSRDLKTAIEKTORGGLSNVGRASIVTKNFFS 385
 Db 860 TMGRIRIVKSIINVGPA---LETFVGD-DINTIL-----ILNLFSGTEYSVKVPAS 906
 Qy 386 KANG---NRSGAPNVVVWVGWPTDKVEASRLAR---ESGINIFETIEGAENEMKQY 439
 Db 907 YSTGFSDALGVAKTLVGLVNTLDYQVRMTSLCAQOLRHATATVAVIESLVGKKQ- 965
 Qy 440 VVEBNFANKAVCRTNGYSL--HVQSWFGLHKTLO----- 472
 Db 966 --EVNLGG-GVPR-HCFEELMPGTEYKISVHAQOEIEGPAVSIMETTLPPPTQPTSPS 1021
 Qy 473 -----PLVKRYCDTRLACSKTCLNSADIGVIDSSVGNFRVTLQFVTNLTKE 524
 Db 1022 TTLPPPTIPPAKEVCKAAK-----ADLVFLVDSMSIGDDNFNKIISFLYSTVGA 1071
 Qy 525 FE-ISDITRIGAVQYTYEORLEFGFDKYSKPDILNAIKRVGYWSGTSGAALNFAL 583
 Db 1072 LDKTGPDTQVAIIQFSDDPRTFELNAYKTKETLLEAIQIAYKGGNTGKAIKHARE 1131
 Qy 584 QLF-----KSKRNKRKMLITLDGSRSDVAVIPAMAHLKGVITVAIGVAMAQOELE 637
 Db 1132 VLFPGAGMKRGKIP---KVLVVIITDGSQDDVKNVSRMQLDGFSPFALGVADADYSELV 1188
 Qy 638 VIATHPARDSFFVDFEDNHLQVPRRIQNIC 669
 Db 1189 NIGSKPSEBHVFFVDDPDAFTKIEDLITFVC 1220

RESULT 9

collagen alpha 1(VII) chain precursor - human

N/Alternate names: procollagen alpha 1(VII) chain

C/Species: Homo sapiens (man)

C/Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 09-Jul-2004

C/Accession: A54849; PH0844; S16316; I56328; A30296; I84686

R/Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.

J. Biol. Chem. 269, 20256-20262, 1994

A/Title: Cloning of human type VII collagen. Complete primary sequence of the alpha(VII)

A:Reference number: A54849; MUID:94327588; PMID:8051117
A:Accession: A54849
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2944 <CHR>
A:Cross-references: UNIPROT:002388; UNIPARC:UPI000017A138; GB:L02870; NID:987124; PIDN:R:Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
A:Title: Molecular cloning and characterization of type VII collagen cDNA.
A:Reference number: PH0844; MUID:92231902; PMID:1567409
A:Accession: PH0844
A:Molecule type: mRNA
A:Residues: 'ERR',340-475, 'PALTASHSTLCWRATRWHPNCRSGHWTRACPCNRPASHARARAG',524-528, 'C',
A:Cross-references: UNIPARC:UPI000017A139; DDBJ:D11152; DDBJ:D13694; NID:9453698; PIDN:E
A:Experimental source: keratinocyte
A:Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
R:Parente, M.G.; Chung, L.C.; Rysaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Maer
proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A:Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A:Reference number: S16316; MUID:91334380; PMID:1871109
A:Accession: S16316
A:Molecule type: mRNA
A:Residues: 815-892, 'E',894-1439 <PAR>
A:Cross-references: UNIPARC:UPI000016A722; GB:M65158; GB:549017; NID:gl80914; PIDN:AAA96
A:Experimental source: keratinocyte
R:Gammon, W.R.; Abernethy, W.L.; Pedilla, K.M.; Prisyamb, P.S.; Cook, M.E.; Wright, J.;
J. Invest. Dermatol. 99, 691-696, 1992
A:Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot
A:Reference number: I56328; MUID:93107742; PMID:1469284
A:Accession: I56328
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'ERR',372-517, 'DV',520-540, 'W',542-1255 <RES>
A:Cross-references: UNIPARC:UPI000016B3AC; GB:S51236; NID:9262308; PIDN:AAB24637.1; PID:
R:Selzler, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E
J. Biol. Chem. 264, 3822-3826, 1989
A:Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagenase
A:Reference number: A30296; MUID:89139437; PMID:2537292
A:Accession: A30296
A:Molecule type: protein
A:Residues: 'A',1240-1246, 'G',1248-1250, 'XE',1253-1255, 'Q',1257, 'E',2032, 'C',2034-2041;
A:Cross-references: UNIPARC:UPI000017A13A; UNIPARC:UPI000017A13B; UNIPARC:UPI000017A13C;
A:Note: two reported peptides cannot be reliably located
R:Greenspan, D.S.
Hum. Mol. Genet. 2, 273-278, 1993
A:Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A:Reference number: I48103; MUID:99271985; PMID:8499916
A:Accession: I48103
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 2395-2871, 'S',2873-2944 <RE2>
A:Cross-references: UNIPARC:UPI000016A724; GB:L06862; NID:g388713; PIDN:AAA89196.1; PID:
R:Christiano, A.M.; Rysaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A:Reference number: A55255; MUID:94224777; PMID:8170945
A:Contents: annotation
A:Comment: Prolines and lysines at the third position of the tripeptide repeating unit (e
ed and subsequently O-glycosylated.
C:Genetics:
A:Gene: GDB:COL7A1; EBRI; EBD1; EB
A:Cross-references: GDB:128750; OMIM:120120
A:Map position: 3p21.3-3p21.3
A:Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
C:Complex: type VII collagen is probably a homotrimer
C:Function:
A:Description: structural component of extracellular polymer associated with anchoring f
A:Keywords: coll'd coll.; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolin
F:1-16/Domains: signal sequence #status predicted <SIG>
F:17-2944/Product: collagen alpha 1 (VII) chain #status predicted <MAT>
F:17-1253/Domains: amino-terminal nonhelical #status predicted <NC1>
F:36-201/Domains: von Willebrand factor type A repeat homology <WAI>

Query Match

| Best Local Similarity | 9.4% | Score 329.5; | DB 2; | Length 2944; |
|-----------------------|------------------|----------------|------------|--------------|
| Matches | 80; Conservative | 37; Mismatches | 88; Indels | 19; Gaps |

4; DB 59

QY 470 TIOPVLKRC-----DTDLRACSKTCLNSADIGFVLDSSSVGTGNFRYLQ 516
|||::|||:
2 TLRLLVALCAGLAPRVRAQHREVTCTR--LYAADIVFLDGSISIRSNPREFRS 59

QY 517 FVTNLTKEFE--ISDPTDRIGAVOYTVEQRLEFGFDKYSSKPDIILAKRVGWSGGTST 574
|-:::-
Db 60 FLEGTLVPESGAASAGVPRATGVQSDDPRTFERGLDALSGSDGVRIAIRRELTSYKCGNTRT 119

QY 575 GAALNALAQQLF--KSKPKRKMLMILTGRSVDVPRIPMAHLKGVIITVAAGVAAA 632
|||||:
Db 120 GAAILHVAHVHVFPLQARPPVPVKCILITDGKSDDLVDTAQRKLKGQVKLFVAGIKNAD 179

QY 633 OELEVIATHPARDHSFVDEFDNLHQVPRIIIONICTEFNSQP 676
|||:::-
Db 180 PEELKRVASQPSIDFFPVNDPFSLRTLRLPLVSRKVCTTAGGPV 223

RESULT 10

A45974

collagen alpha 1 (XIV) chain precursor, short form 2 - chicken

N.Alternate names: undulin

C.Species: Gallus gallus (chicken)

C.Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text_change 09-Jul-2004

R.Accession: A45974; S30085; S22913; S17035; S20833

R.Character: D.R.; Foley, J.W.; Castagnola, P.; Gemari, M.; Dublet, B.; Cancedda, R.; Lin

J.Biol.Chem. 268, 12177-12184, 1993

A.Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region

nb.

A.Reference number: A45974; WUID:93280195; PMID:8505337

A.Accession: A45974

A.Status: preliminary

A.Molecule type: mRNA, protein

A.Residues: 1-1747 <GER>

A.Cross-references: UNIPROT:P32018, UNIPARC:UPI0000173C47

A.Experimental source: embryo skin

A.Note: sequence inconsistent with the nucleotide translation

A.Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBIP:133365)

R.Abpe, S.S.
submitted to the EMBL Data Library, March 1992

A.Reference number: S30085

A.Accession: S30085

A.Molecule type: mRNA

A.Residues: 1472-1660 <APT>

A.Cross-references: UNIPARC:UPI00000006A2; EMBL:X65122; NID:g62871; PID:CNA446238.1; PID:R1rueb, J.; Tueb, B.

Eur. J. Biochem. 207, 549-557, 1992

A>Title: Type XIV collagen is a variant of undulin.

A|Reference number: S22916; MUID:92339443; PMID:1393349

A|Accession: S22916

A|Status: preliminary

A|Molecule type: mRNA

A|Residues: 286-499, 'O', 496-834, 'A', 836-1119, 'K', 1122-1402, 1409-1439 <TRU>

A|Cross-references: UNIPARC:UPI0000173C48

R|Gordon, M.K.; Catagnola, P.; Dublet, B.; Linsmeayer, T.F.; van der Rest, M.; Mayne, Eur. J. Biochem. 201, 333-336, 1991

A|Title: Cloning of a cDNA for a new member of fibrin-associated collagens

A|Reference number: S17035; MUID:92037585; PMID:1935930

A|Accession: S17035

A|Molecule type: mRNA

A|Residues: 1472-1659 <GOR1>

A|Cross-references: UNIPARC:UPI0000173C49

A|Accession: S20833

A|Molecule type: protein

A|Residues: 1551-1570; 1593-1599; 1639-1667 <GOR2>

A|Cross-references: UNIPARC:UPI0000173C49

C|Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trim

F|40-204/Domain: von Willebrand factor type A repeat homology <WMA1>

F|236-317/Domain: fibronectin type III repeat homology <FN3A>

F|326-409/Domain: fibronectin type III repeat homology <FN3B>

F|418-498/Domain: fibronectin type III repeat homology <FN3C>

F|507-591/Domain: fibronectin type III repeat homology <FN3D>

F|626-707/Domain: fibronectin type III repeat homology <FN3E>

F|716-798/Domain: fibronectin type III repeat homology <FN3F>

F|806-893/Domain: fibronectin type III repeat homology <FN3G>

F|924-1089/Domain: von Willebrand factor type A repeat homology <VMA2>

F|1111-1353/Domain: non-collagenous NC4 #status predicted <NC4>

F|1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>

F|1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 9 4% Score 329; DB 2; Length 1747;
Beet Local Similarity 24.8%; Pred. No. 2e-13; Indels 140; Gaps 24;
Matches 142; Conservative 74; Mismatches 216;

Oy 174 IPGTTAQVTTLQMLAVTVAATPTLLPRPSPSASTSIIRPOSVGHRSGEMD----- 227
Db 597 IVGTTAIFTT-----VTTTTTTATTTPKPIIAVRT-----GVRNLVIDDETSS 641

Oy 228 ---LWSTATYTSNQNR-----PRADPGIORQDPSCAAQKPVGADVSLGLVPKEELS 276
Db 642 LRVVWDIDSDHNAQQFRVTVYTAKGDRABEAIMVPGRONTLLQP-----LPDETYX 693

Oy 277 TGSL-----EPVSIGDENCKRIDSLFDGSTSIGKRFRRIQKOLLADVAQLDIGAPGP 330
Db 694 VTITPIYADGEVSVSABQKTPLPS-----APRLRLRSDEVYNNLRISMW-APPSP 743

Oy 331 LMG--VVOYGDN---PATHPNLKTHNSRDLTALTEIKTORGGLSNVGRAISPYTKNFFS 385
Db 744 TMGYRIYKKSINVPGA---LETFVGD-DINTIL-----ILNFLSGTEYSVKVFAS 790

Oy 386 KANG---NRSGAPNVVVVMVDGMPIDKYEBSRLAR---ESGINIFTIIGAENENKOY 439
Db 791 YSTGSDAALTGAKTLYGVTNLDITYOVWRMTSLCAQOMOLHRHARTRYRVALLSLVDKKQ- 849

Oy 440 VPEPFANKAVACRTNGFYSL--HVQSWFGKLHKTIQ----- 472
Db 850 --EVNLGG-GVPR-HCFELMPGTEYKISVHAQOEITCGPAVSIMETTLPPPOPTSPS 905

Oy 473 -----PLYKRVCDTRLACSKTCLNSADIGFIYIDSSSVGNGNFPTVQAFTNLTKE 524
Db 906 TTLPEPTIPPAKEYCAAK-----ADLVFLVDSWSISGDNFKIISFLYSTVGA 955

Oy 525 FE-ISDTRTICAGVAYTEQRLEFGFDKYSSKPDLIINAIKVWGWSGCTSGAIINFALFE 583
Db 956 LDKGPDDQTQVAIIIOFSDDPRTEPKUNAYKTKETILEAIQOIAYKGGTKTKGXIKARE 1015

Oy 584 QLF-----KSKPKRKLMILLITDGSRSYDVRLIPAMAHLKGVITVAINGVAMAAQEELLE 637
Db 1016 VLFGEGAMRGKGIIP---KVLVVITDGRSQDDVNKNKSRSMQMDGSEFFAIVGADADYSELV 1072

| | | | |
|----|------|----------------------------------|------|
| QY | 638 | VIATHPARDHSFVDEPDNLHQVPRRIQNIC | 669 |
| Db | 1073 | NIGSKPSERHVFVDFDFAFTKIEDELITTFVC | 1104 |

RESULT 11
T28797

hypochemical protein C16E9.1 - *Caenorhabditis elegans*
 C1Species: *Caenorhabditis elegans*
 C1Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C1Accession: T28797
 R1Accession: T28797
 submitted to the EMBL Data Library, November 1995
 A1Description: The sequence of C. elegans coemid C16E9.
 A1Reference number: Z20525
 A1Accession: T28797
 A1Status: preliminary; translated from GB/EMBL/DBJ
 A1Molecule type: DNA
 A1Residues: 1-567 <GFI>
 A1Cross-References: UNIPROT:Q18048, UNIPARC:UPI000007PCE4, EMBL:U39677, PIDN:AACT7957.1
 A1Experimental source: Strain Bristol N2; clone C16E9
 C1Genetics:
 A1Gene: CESP:C16E9.1
 A1Map position: X
 A1Introns: 15/3; 77/3; 132/1; 185/3; 231/1; 271/2; 301/2; 430/3; 509/1

| | | | | |
|-----------------------|------------------|--------------------|-------------|-------------|
| Query Match | 9.0% | Score 314.5; | DB 2; | Length 567; |
| Best Local Similarity | 22.0% | Pred. No. 3.5e-13; | | |
| Matches 130; | Conservative 84; | Mismatches 213; | Indels 163; | Gaps 20; |

| | | | | | | | | | | |
|----|-----|--------------------------------------|-----------------------------|----------------------------------|-----------------|------------|---------------|-------------|-----|-----|
| QY | 172 | PRIPGTAQPTLWQLLAVTAVATPTLPSP-SAASTSI | PRPOSVGHRSQEMDLMWS | 230 | | | | | | |
| Db | 37 | PPMP----- | PTDPEGYDDSI | FDITTPTPAPPSNGLRAPMPKMT | 75 | | | | | |
| QY | 231 | TATYTSQNRP----- | RADPG:QRDP | SGAFAQKPVGADVSLGLVPKEELSTQSL | 280 | | | | | |
| Db | 76 | OEIPKESGGQKLTIEDVVGNNIDSHVEVNGSGSDPT | EGSGSDKSGTESEFPASGECA | 135 | | | | | | |
| QY | 281 | EPVSLG----- | PNC | KIDSLFIDGSTSGKRRFRQKDLADVAQALDGP | 327 | | | | | |
| Db | 136 | QGDSLPDMKAMDBEAYLVGNCPSDII | IFVDA | TSV-RGIFEGYITIEKRVVEGLVOP | 194 | | | | | |
| QY | 328 | AGPLMGVVOYGD--NPATHE | NLKTHTNSRDLKTAIEKITORGSLN | GRAISFVTKNFP | 385 | | | | | |
| Db | 195 | TVDHVGAIVSSEKKQTKIKLGEHKRGSLVAVD | LLPFSG | TATGQALKFAAH--- | 251 | | | | | |
| QY | 386 | KANGNRGAPVVVVVWDG | MPTDKVEEASRLARESGIN | IFFITTEGAEN | EKOYVEPNF | 445 | | | | |
| Db | 252 | -TEGRRE | NFTLVYILTDGYSYDLIESGARVLR | E----- | VPNS | 288 | | | | |
| QY | 446 | ANKAVCR | TNGYSLSLHVS | WFGHLTKLQ----- | PLVGR-- | VCDDT----- | 481 | | | |
| Db | 289 | A----- | IYAVISGEIF-LRKE | LEMITGNPDNVL | TGMSYGTLLVRLKLC | CAPIKAA | 338 | | | |
| QY | 482 | ----- | DRLACS----- | ----- | KTCLNSADIGF | 498 | | | | |
| Db | 339 | TLKQSN | RGVLVRPGFSLDRFOHRSRLTANLEAK | HTGTDVFKTP | KEKRPVDCI-- | YDIGI | 396 | | | |
| QY | 499 | VIDGSS | SVGTGNFTVLQFV | TNLTKEFEISD | TTRIGAVOY | YEQRL | EPFGDKYSSK | 558 | | |
| Db | 397 | IFDSSG | SL-EKNFQKOLAF | AKOLVEQMPIDSN | ATRVGIVQ | PAC | KTKRVLANFSONK | 558 | | |
| QY | 559 | LNAIK | RGVNGGCGTGA | AINFALEOLF | FKSK-- | PNK | KMLILITDGS | YDVRIPAAAH | 617 | |
| Db | 456 | KTIIDR | SPFVS | GGTFTFQALK-KMA | ALYESKRN | NALKML | LLFDG | ISADTSEGEAL | 514 | |
| QY | 618 | LKG | YTAIGV----- | AMAOE | LEVIATPHARD | HSFV | DEFDNL | HOYVP | 662 | |
| Db | 515 | SGV | VYTVTGISTDKS | AGLNKEL | RGMT-- | SS | HHYDSSD | FADLLH | GFP | 562 |

RESULT 12

A/Cross-references: UNIPARC:UPI000016B30B; GB:M60675; NID:g340357; PIDN:AAA61295.1; PID:
 A/Note: the authors translated the codon CGC for residue 156 as Gln
 R/Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagian,
 Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987
 A/Title: Molecular cloning of the human gene for von Willebrand factor and identification
 A/Reference number: 523676; MUID:87260814; PMID:3436594
 A/Accession: 523676
 A/Molecule type: DNA
 A/Residues: 2731-2813 <COL>
 A/Cross-references: UNIPARC:UPI000014240A; EMBL:M16945
 R/Bonthron, D.; Orr, E.C.; Miesock, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.
 Nucleic Acids Res. 14, 7125-7127, 1986
 A/Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.
 A/Reference number: A25298; MUID:87016349; PMID:3489923
 A/Accession: A25298
 A/Molecule type: mRNA
 A/Residues: 1-470, 'V', 472-2813 <BON>
 A/Cross-references: UNIPARC:UPI000017431B; EMBL:X04385
 R/Verweij, C.L.; Diegaarde, P.J.; Hart, M.; Pannekoek, H.
 EMBO J. 5, 1839-1847, 1986
 A/Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive protei
 A/Reference number: A91044; MUID:87004550; PMID:3019665
 A/Accession: A25469
 A/Molecule type: mRNA
 A/Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>
 A/Cross-references: UNIPARC:UPI000017431C; EMBL:X04146
 A/Note: this sequence has been revised in reference A91056
 R/Verweij, C.L.; Diegaarde, P.J.; Hart, M.; Pannekoek, H.
 EMBO J. 5, 3074, 1986
 A/Reference number: A91056
 A/Accession: A25366
 A/Molecule type: mRNA
 A/Residues: 1021-1030 <VE2>
 A/Cross-references: UNIPARC:UPI000017431D
 A/Note: this is a revision to the sequence from reference A91044
 R/Shelton-Inloes, B.B.; Broze Jr., G.O.; Miletich, J.P.; Sadler, J.E.
 Biochem. Biophys. Res. Commun. 144, 657-665, 1987
 A/Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repeated
 A/Reference number: 523618; MUID:87213253; PMID:3495266
 A/Accession: 523618
 A/Molecule type: mRNA
 A/Residues: 1-120 <SH2>
 A/Cross-references: UNIPARC:UPI000016B30A; EMBL:M17588; NID:g799330; PIDN:AAA65940.1; PI
 A/Accession: 523645
 A/Molecule type: protein
 A/Residues: 23-56 <SH3>
 A/Cross-references: UNIPARC:UPI000017431E
 R/Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie, E.W
 Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985
 A/Title: Cloning and characterization of two cDNAs coding for human von Willebrand fact
 A/Reference number: A94060; MUID:86016708; PMID:2864688
 A/Accession: A94060
 A/Molecule type: mRNA
 A/Residues: WA, 739, 'C', 744-769, 'H', 771-788, 'A', 790-803, 'S', 805-873, 1289-1471, 'D', 1473-
 A/Cross-references: UNIPARC:UPI000017431F; UNIPARC:UPI0000174320
 A/Note: the authors translated the codon TCG for residue 2168 as Cys
 R/Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.
 Biochemistry 25, 3164-3171, 1986
 A/Title: cDNA sequences for human von Willebrand factor reveal five types of repeated dc
 A/Reference number: A90504; MUID:86265894; PMID:3488076
 A/Accession: A90504
 A/Molecule type: mRNA
 A/Residues: 781-788, 'A', 790-1424 <SHE>
 A/Cross-references: UNIPARC:UPI0000174321
 R/Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Lact, S.A.; C
 Science 228, 1401-1406, 1985
 A/Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clones
 A/Reference number: A44178; MUID:85244588; PMID:3874428
 A/Accession: A44178
 A/Molecule type: mRNA
 A/Residues: 2821-2813 <GIN>
 A/Cross-references: UNIPARC:UPI000016B307; EMBL:K03028; NID:g340308; PIDN:AAA61293.1; PI

R/Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; van
 Nucleic Acids Res. 13, 4699-4717, 1985
 A/Title: Construction of cDNA coding for human von Willebrand factor using antibody probe
 A/Reference number: 507363; MUID:85269603; PMID:3875078
 A/Accession: 507363
 A/Molecule type: mRNA
 A/Residues: 2731-2813 <VE3>
 A/Cross-references: UNIPARC:UPI000014240A; EMBL:X02672; NID:g37939; PIDN:CAA26503.1; PID
 R/Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Living
 Cell 41, 49-56, 1985
 A/Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by a r
 A/Reference number: 523678; MUID:85201687; PMID:3873280
 A/Accession: 523678
 A/Molecule type: mRNA
 A/Residues: 2731-2813 <LYN>
 A/Cross-references: UNIPARC:UPI000014240A; EMBL:X03028
 R/Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.;
 Biochemistry 25, 3171-3184, 1986
 A/Title: Amino acid sequences of human von Willebrand factor.
 A/Reference number: A90505; MUID:86269895; PMID:3524673
 A/Accession: A90505
 A/Molecule type: protein
 A/Residues: 764-788, 'A', 790-1471, 'D', 1473-2813 <TIT>
 A/Cross-references: UNIPARC:UPI0000174322
 A/Note: 789-Thr was also found
 R/Chopek, M.W.; Girma, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.
 Biochemistry 25, 3146-3155, 1986
 A/Title: Human von Willebrand factor: a multivalent protein composed of identical subunit
 A/Reference number: A23464; MUID:86269892; PMID:3015199
 A/Accession: A23464
 A/Molecule type: protein
 A/Residues: 764-773, 2803-2813 <CHO>
 A/Cross-references: UNIPARC:UPI0000174323; UNIPARC:UPI0000174324
 R/Dent, J.A.; Berkowitz, S.D.; Ware, J.; Kaeper, C.K.; Ruggeri, Z.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990
 A/Title: Identification of a cleavage site directing the immunohemical detection of mole
 A/Reference number: A36013; MUID:90349604; PMID:2385594
 A/Accession: A36013
 A/Molecule type: protein
 A/Residues: 1606-1617 <DEN>
 A/Cross-references: UNIPARC:UPI0000174325
 R/Evy, P.U.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B.M.;
 Science 233, 995-998, 1986
 A/Title: Propylpeptide of von Willebrand factor circulates in blood and is identical to
 A/Reference number: A60913; MUID:86208144; PMID:3486471
 A/Accession: A60913
 A/Molecule type: protein
 A/Residues: 576-590 <FAV>
 A/Cross-references: UNIPARC:UPI0000174326
 C/Genetics:
 A/Gene: GDB:WVF
 A/Cross-references: GDB:119125; OMIM:193400
 A/Map position: 12p13.3-12p13.2
 A/Intons: 19/1, 74/1, 108/2, 178/1, 219/3, 292/1, 333/1, 370/2, 386/1, 431/3, 478/1, 511
 5/1, 1724/1, 1771/1, 1819/1, 1874/1, 1888/3, 1948/1, 2021/3, 2086/1, 2200/1, 2266/3, 2203
 C/Superfamily: von Willebrand factor; von Willebrand factor A repeat homology; von v
 C/Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicat
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 F:23-763/Product: von Willebrand antigen II #status predicted <WA1>
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 F:387-745/Domain: type D repeat 2 <DD2>
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 F:764-2813/Product: von Willebrand factor #status predicted <WA2>
 F:784-865/Domain: D' <DDD>
 F:788-833, 2216-2261/Region: duplication
 F:826-853, 2400-2515, 2544-2662/Region: duplication
 F:842-1130, 1934-2203/Region: duplication
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 F:1496-1654/Domain: von Willebrand factor type A repeat homology <VWA2>
 F:1689-1854/Domain: von Willebrand factor type A repeat homology <VWA3>
 F:1947-2295/Domain: type D repeat 4 <DD4>
 F:2296-2330/Domain: type B repeat 1 <VB1>

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 7, 2006, 01:31:57 ; Search time 16 Seconds
(without alignments)
490.073 Million cell updates/sec

Title: US-10-063-540-34
Perfect score: 3502
Sequence: 1 MRLVLTMKASVIEMLVL.....QYVRIITQICTEFNQPRN 678

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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- 8: /EMC_Celerra_SIDS3/prodata/2/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 3502 | 100.0 | 678 | 6 US-10-196-749-150 | Sequence 150, App |
| 2 | 3502 | 100.0 | 678 | 7 US-11-101-316-34 | Sequence 34, Appl |
| 3 | 1129.5 | 32.3 | 550 | 6 US-10-196-749-46 | Sequence 46, Appl |
| 4 | 232 | 6.6 | 180 | 1 US-09-970-076-3 | Sequence 3, Appl |
| 5 | 231 | 6.6 | 1152 | 6 US-10-511-937-2444 | Sequence 2444, Ap |
| 6 | 204.5 | 5.8 | 436 | 6 US-10-505-928-592 | Sequence 592, App |
| 7 | 203.5 | 5.8 | 1170 | 6 US-10-511-937-3007 | Sequence 3007, Ap |
| 8 | 193 | 5.5 | 1151 | 7 US-11-246-999-103 | Sequence 103, App |
| 9 | 192.5 | 5.5 | 1034 | 7 US-11-246-999-43 | Sequence 43, Appl |
| 10 | 192.5 | 5.5 | 1189 | 7 US-11-246-999-35 | Sequence 35, Appl |
| 11 | 190.5 | 5.4 | 437 | 7 US-11-293-697-3386 | Sequence 3386, Ap |
| 12 | 170.5 | 4.9 | 198 | 1 US-10-196-749-70 | Sequence 70, Appl |
| 13 | 143.5 | 4.1 | 500 | 6 US-10-196-749-46 | Sequence 46, Appl |
| 14 | 133.5 | 3.8 | 524 | 7 US-11-293-697-3442 | Sequence 3442, Ap |
| 15 | 131.5 | 3.8 | 247 | 7 US-11-330-353-4 | Sequence 4, Appl |
| 16 | 113.5 | 3.2 | 405 | 6 US-10-953-349-1810 | Sequence 1810, Ap |
| 17 | 113.5 | 3.2 | 422 | 6 US-10-953-349-1809 | Sequence 1809, Ap |
| 18 | 113.5 | 3.2 | 411 | 6 US-10-953-349-1808 | Sequence 1808, Ap |
| 19 | 112 | 3.2 | 231 | 7 US-11-293-697-4167 | Sequence 4167, Ap |
| 20 | 111.5 | 3.2 | 382 | 6 US-10-953-349-24980 | Sequence 24980, A |
| 21 | 110 | 3.1 | 338 | 6 US-10-953-349-5351 | Sequence 5351, Ap |
| 22 | 110 | 3.1 | 352 | 6 US-10-953-349-5350 | Sequence 5350, Ap |
| 23 | 108.5 | 3.1 | 681 | 6 US-10-953-349-10919 | Sequence 10919, A |
| 24 | 108 | 3.1 | 422 | 6 US-10-953-349-26025 | Sequence 26025, A |
| 25 | 107 | 3.1 | 880 | 6 US-10-953-349-6391 | Sequence 6391, Ap |

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|----|-------|-----|------|-----------------------|-------------------|
| 26 | 105 | 3.0 | 354 | 6 US-10-953-349-28519 | Sequence 28519, A |
| 27 | 103.5 | 3.0 | 577 | 7 US-11-293-697-3929 | Sequence 3929, Ap |
| 28 | 103 | 2.9 | 334 | 7 US-11-293-697-3527 | Sequence 3527, Ap |
| 29 | 102 | 2.9 | 409 | 6 US-10-953-349-32547 | Sequence 32547, A |
| 30 | 102 | 2.9 | 652 | 6 US-10-953-349-5551 | Sequence 5551, Ap |
| 31 | 102 | 2.9 | 693 | 7 US-11-293-697-3849 | Sequence 3849, Ap |
| 32 | 101 | 2.9 | 326 | 6 US-10-953-349-17338 | Sequence 17338, A |
| 33 | 101 | 2.9 | 343 | 6 US-10-953-349-17337 | Sequence 17337, A |
| 34 | 101 | 2.9 | 350 | 6 US-10-953-349-17336 | Sequence 17336, A |
| 35 | 100.5 | 2.9 | 314 | 7 US-11-293-697-2665 | Sequence 2665, Ap |
| 36 | 100.5 | 2.9 | 769 | 6 US-10-522-043-9 | Sequence 9, Appl |
| 37 | 100 | 2.9 | 333 | 1 US-09-970-076-8 | Sequence 8, Appl |
| 38 | 100 | 2.9 | 368 | 1 US-09-970-076-2 | Sequence 2, Appl |
| 39 | 100 | 2.9 | 564 | 1 US-09-970-076-6 | Sequence 6, Appl |
| 40 | 99.5 | 2.8 | 915 | 6 US-10-523-014-4 | Sequence 4, Appl |
| 41 | 99 | 2.8 | 335 | 6 US-10-953-349-25256 | Sequence 25256, A |
| 42 | 99 | 2.8 | 338 | 6 US-10-953-349-24981 | Sequence 24981, A |
| 43 | 98.5 | 2.8 | 384 | 6 US-10-505-928-395 | Sequence 395, App |
| 44 | 98.5 | 2.8 | 4373 | 7 US-11-118-524-2 | Sequence 2, Appl |
| 45 | 97.5 | 2.8 | 222 | 6 US-10-953-349-27868 | Sequence 27868, A |

ALIGNMENTS

RESULT 1
US-10-196-749-150
Sequence 150, Application US/10196749
Publication No. US200609486441
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196, 749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 150
LENGTH: 678
TYPE: PRT
ORGANISM: Homo Sapien
US-10-196-749-150

Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 4,3e-235;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 301 STSIGKRFRIOQLADVAQALDIGPAGPLMGVVOYGDNPATHFNLKHTNSRDLKTAI 360
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QY 601 TDRGSYDVARIPMAAHLKGVITYAIGVMAAEOELEVIATHPARDSFFVDEFDNLHOY 660
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RESULT 2

US-11-101-316-34
; Sequence 34, Application US/11010316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 34
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-34

Query Match 100.0%; Score 3502; DB 7; Length 678;
Best Local Similarity 100.0%; Pred. No. 4,3e-235;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 661 VPRIONICTEFNSQPRN 678
DB 661 VPRIONICTEFNSQPRN 678
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RESULT 3

US-10-196-749-46
; Sequence 46, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deanoysers, Inc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zheng, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 46
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-196-749-46

Query Match      32.3%; Score 1129.5; DB 6; Length 550;
Best Local Similarity 37.1%; Pred. No. 5.4e-71;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

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DB 32 ITCTTRGIDIRKEDADVLCFPGCCPLEERSYVGNIVYASVSSICGAAYHKGVIINSGGFVR 91
QY 104 VRKVAAGSGYKGSYVNGVOSLSLPRWRESFVLESKPKKGVTPREALTYSSKSPAAQAG 163
DB 92 VYSLPGRENYSVANGIOSQMLSRMSASFTYTKGK-----SSTQETQGA- 137
QY 164 ETTAAVQRPPIPGTTAOPVTLMQLLAVVAATPTTLRPSBSAASTISIRPQSVGHS 223
DB 138 -----VSTAH----- 143
QY 224 QEMDLWSTATYTSQNRPRADPGIORDPGSAAPQKPVGADVSLGLVPEKEELSTQSLBPV 283
DB 144 -----PTGKRLK-----TPKK----- 156
QY 284 SLGDPNCKIDSLFIDGSTSGKRRFRIQKQLLDVAQALDIPGAPLMGVVQGDNPAT 343
DB 157 -TGKMDCKADIAFLIDGSFNIGRRFNLQKVFVKVALLMIGITGEPHVGVLQASEHPKI 215
QY 344 HFNKLTHTNSRDLKTAIEKITQKGLSVNGRAISVTTNPFSSKANGNSGAPNVVVVWD 403
DB 216 EFTYKNTFSADVFLAKEVGFRGNSNTGALKKHTAKPFTVADGVRKGIPKVVVVVID 275
QY 404 GMPFDKVEASRLARESGINIFITIEGAENKQYVVEPRFANKAVCRITNGFYSLAVOS 463
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DB 276 GMPSDDIEEAGIVAREGVNVFIVSAKPIDEELGMVDVTVKAVCRNNGFFSYHMPN 335
QY 464 WFGHLKTLQPLVKVSCOTDLRACGKTCUNSDIGFVIDGSSVGNNGRTVLOFVNTLK 523
DB 336 WFGTKYKVPLOVQKCTHEQOMCKSKTCVNSVNIAPFLIDGSSVGDNSRNLWLEFVSNIAK 395
QY 524 EFEISDTRIGAQVYTEQRLFEFGFDKSSKPDILNAIKRVGWSGGSTGAAINFALE 583
DB 396 TFEISDIGAKIAAQVFTDQRTFSFTDYSKENVLAIVIRNIRVMSGGTATGDAISFTVR 455
QY 584 QLFK--KSKPKRKMLLITDGRSYDVRIRPAAAHKGVITVYALGVMAAOELEVAT 641
DB 456 NVFPIRESPMK-NFLVIVTDGQSYDDVQGPAAAHADAGITFISGVAMAPLDDLKOWAS 514
QY 642 HPARDHSFVDEPNLHQVPRILIONCTEF 672
DB 515 KPESHAFETREFTGLEPIVSDVIRGICRDF 545

RESULT 4
US-09-970-076-3
; Sequence 3, Application US/09970076
; Publication No. US20060110801A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Anthrax Toxin Receptor
; FILE REFERENCE: 960296.97745
; CURRENT APPLICATION NUMBER: US/09/970,076
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/0251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: von Willebrand
; OTHER INFORMATION: Factor A domain consensus sequence
US-09-970-076-3

Query Match      6.6%; Score 232; DB 1; Length 180;
Best Local Similarity 32.0%; Pred. No. 1.5e-09;
Matches 48; Conservative 38; Mismatches 60; Indels 4; Gaps 2;

QY 292 IDLSFLIDGSTSGKRRFRIQKQLLDVAQALDIPGAPLMGVVQGDNPATHTLTKHT 351
DB 2 LDVVFLLDGSQSGMGNFELKEFVLKLVLEQDLIGPRDVRGLVTFSSDAVLEPLDNDQ 61
QY 352 NSRDLKTAIEKIT-QRGGLSVNGRAISVTTNPFSSKANGNSGAPNVVVVWDGMPFDKV 410
DB 62 SKDALLERLANLSTSLGGTTLGAALEALENLSEBSAGSRGAPKVLILITDDESNDG 121
QY 411 EASRLARE--SGINIFITIEGAENK 437
DB 122 EDILKAKEKLRSGVKVFVVGAVDDEE 151

RESULT 5
US-10-511-937-2444
; Sequence 2444, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
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; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2444
; LENGTH: 1152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2444
```

Query Match 6.6%; Score 231; DB 6; Length 1152;

Best Local Similarity 33.0%; Pred. No. 2.5e-08;

Matches 62; Conservative 39; Mismatches 63; Indels 24; Gaps 7;

```

QY 494 ADIGFVLDSSSVGTGNFRTVLOFVNLTKFEISDTRIGAVQYTEORLEFGPKYS 553
DB 149 SDIAFLIDGSGSITPHDFRKRKEFVSTVME--QLKSKTTLFSLMOSEEFHHTFEFQ 206
QY 554 SKPDILNAIKRVGWSGSGTGAALNPALEOLF--KSKPKRKLMLITDGR----- 604
DB 207 NNPNRSLVVPITQLGRTHTATGIRKRVHLEFNITGARNAPKILVIVIDGSKFGDPL 266
QY 605 SYDDVRTPMAAHLKGVITTAIGVAAA-----AOEEVLATHPADHSFVDFEDNLHQ 659
DB 267 GYEDV-IP--EADREGVIRYVIGVADAFRSEKSRQELNTASKPRDHVFQVNNFEAL-- 321
QY 660 YVPRITON 667
DB 322 ----KTION 326
```

RESULT 6

US-10-505-928-592

Sequence 592, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research et al.

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

FILE REFERENCE: 28967/39178

CURRENT APPLICATION NUMBER: US/10/505,928

CURRENT FILING DATE: 2004-08-27

PRIOR APPLICATION NUMBER: US 60/363,019

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 866

SOFTWARE: Patentin 3.2

SEQ ID NO 592

LENGTH: 436

TYPE: PRT

ORGANISM: Homo sapiens

US-10-505-928-592

Query Match 5.8%; Score 204.5; DB 6; Length 436;

Best Local Similarity 22.0%; Pred. No. 4.2e-07;

Matches 95; Conservative 70; Mismatches 193; Indels 73; Gaps 18;

```

QY 290 CK--IDLSFLIDGSTIGKRRFRIQQLADVAAQALD-----IGPAGPLMGVVOYGDN 340
DB 17 CKGGPDLFLVLDSSSEISIGLQNFELAKDFVKKVIDRLSRDELVKFEFGGSGVAGVVOY--- 73
QY 341 PAFHNLKHTF-----NSRDLKTAIEKITORGGLSNVGRATSPVTKQFFSKANGNRS 392
DB 341 PAFHNLKHTF-----NSRDLKTAIEKITORGGLSNVGRATSPVTKQFFSKANGNRS 392
```

```

DB 74 --SHSQWQEHVSIRSPSIRNVQELKEAIKSLQWMAAGTFTGEALQYTRDQLLPSPNNR- 130
QY 393 GAPVVVVWVDG-WPTKXVEASRLAESGINIFETIEGAAB-----NEKQYVE----- 442
DB 131 ----IALVITDGSSDTRDTPPLANVCSPGIQVSVGIKVPFPIPSDOLNIVSCGGLA 186
QY 443 PNFANKAVCRITNGEYSLHVSQWFGHLAKTLQPLVKRVCDTRLACSKTCLNSADIGFVIG 502
DB 187 PSQGRPGLSLVKENYVABELDAFLKNVTAQICIDKKCPD--YTCPIFFSSPADITLLEP 244
QY 503 SSSVGTGNFRTVLOFVNLTKFEISDT-----DTRIGAVQY--TYEOR-----LERGFD 550
DB 245 PPDVSHNFDTYKFAKRLAERFLTAGRTDPADHVAVVOYSGTGQRPERRASLQF-LQ 303
QY 551 KYSKPDILNAIKRVGWSGSGTGAALNPALEOLF--FKSKPKRKLMLITDGRSYD--- 607
DB 304 NYTR--LASAVDAMPFNATDVNDALGVYTFYREASGGAKKRLLLSDNSQCATP 360
QY 608 -DVRIPMAAHLKGVITTAIGVAAAQOE-ELEVIATHPARD-----HSFVDFEDNL 657
DB 361 AAIEKAVQEAQRAGIEIFVNVVGRQVNEPHIRVLVTGKTAEDVAVAGESHLFVPSYQAL 420
QY 658 ----HQYVPR 663
DB 421 LRGVFHQYVSR 431
```

RESULT 7

US-10-511-937-3007

Sequence 3007, Application US/10511937

Publication No. US20060088836A1

GENERAL INFORMATION:

APPLICANT: EXPRESSION DIAGNOSTICS, INC.

APPLICANT: Kohlgenmuth, Jay

APPLICANT: Fry, Kirk

APPLICANT: Woodward, Robert

APPLICANT: Ly, Ngoc

APPLICANT: Prentice, James

APPLICANT: Macdonald

APPLICANT: Rosenberg, Steven

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

FILE REFERENCE: 506612000104

CURRENT APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117

SOFTWARE: Patentin version 3.2

SEQ ID NO 3007

LENGTH: 1170

TYPE: PRT

ORGANISM: Homo sapiens

US-10-511-937-3007

Query Match 5.8%; Score 203.5; DB 6; Length 1170;

Best Local Similarity 23.8%; Pred. No. 2e-06;

Matches 85; Conservative 57; Mismatches 124; Indels 91; Gaps 14;

```

QY 383 FFSKAN-----GNRSGAP-----NVVVVVWVDGWPDKVEASRLARES 420
DB 19 FFAFPASSYINDVAGNBSFSPPRAGRFGYRVLOVGNQVIV--GATGEGNSTGSLVQCQS 75
QY 421 GI-NIFETIEGAENENKQYVVEPNFANKAVCRITNGEYSLHVSQWFGHLAKTLQPLVKRV 479
DB 76 GTGHCUPVTLRGS-----NYTSKYLQMT-----LATDPDQSIACDPGLSRTC 119
QY 480 DTD-----RLACSKTCLNSADIGVINGSSSVGTGNFRTVLOFV 518
DB 480 DTD-----RLACSKTCLNSADIGVINGSSSVGTGNFRTVLOFV 518
```

```

Db      120 DONTYSLCYLFRONLQGMPLQGRPFQECIKGNVDLFLFDGSMLOPDEFOKILDPM 179
Qy      519 TNLTFEPISTDRIGAVOYTYEORLEFGFDKYS--SKPDLINAIKRGVWSGSTGCA 576
      180 KDVK--KLSTSTQFAAVQSTSTKTEFDSIDYKMKDPDL--LKVKKMLLTNTFG 235
Qy      577 AINFALEOLFVK--SKPNKKMLMLITDGRSYDVRIPAMAHLKGVITTAIGV----- 628
Db      236 AINVAATEVFREELGARDATKVLIIITDGEATDSCNIDA-----AKDIIRYIIGIGKHFQ 291
Qy      629 AMAAOEELVATHPARHSEFFVDFNLHQYVPIIONTI-----CTEFSQ 675
Db      292 TKSOETLHKFASKPASEFVKILDTFEKLDLFTLQKIVIEGTSKODLTSFME 348

```

```

RESULT 8
US-11-246-999-103
; Sequence 103, Application US/11246999
; Publication No. US20060099622a1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-246-999-103

```

```

Query Match      5.5%; Score 193; DB 7; Length 1151;
Best Local Similarity 20.7%; Pred. No. 1.1e-05;
Matches 84; Conservative 59; Mismatches 134; Indels 128; Gaps 13;
Qy      269 LVPKEELSTQSLSPVSLDLPNCKIDLSFLIDGSTSIGRRPRIOQLADVAQALDIPGA 328
      133 IAPVQEGSTQ-----LDIVIVLDGNSI--YPMDSYAFANLILKRDIDPK 177
Qy      329 GPLMGVVOYGDNPATHPNLKTHNSRDILKTAIEKTORGGLSNV--GRAISFVTKNPFKA 387
      178 QTVGIVVOYGENVTHFEFLNKYSTEEVLVAAKIVQGGROTALGTARKEAFTEA 237
Qy      388 NGNRSGAPNVVWVDGWPDT--KVEEASRLARESGINIFITTEGA-----AE 434
      238 RGAARGVKVWVITVDGSHNHLKVKYIQDCEDENIQRFISALIGSYNRGNLSTEKFE 297
Db      435 NEKOYVPE--NFANKAVCRITNGFYSLHVSWMFLHKTLOPLVRCVDTDLRLACSKTCL 491
      298 EIKSIASEPTEKHFN-----VDELALVITVITLGERI----- 331
Qy      492 NSADIGVIVDSSSVGTGNFTVLQFTNLTKFEPISTDRIGAVOYTYEORLEFGDK 551
      332 -----FALEATVADQSAASF-----EMEMSQT-----GRSA 356
Qy      552 YSSKPDILNAIKRGVWSGSTGAA-----INFALQLFKSKRNKMKMLILTDG 603
      357 HYSODWMLGAVGAYDMNGTVVMOKASQIILPRNTTFVEST--KKNP----- 403

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Qy      604 RSYDVRIPAMAHLKGVITTAIGVAMAAOEELVIAHPARDHS 648
Db      404 -----LASYLGYTVNSATASGSDVLYIAGQPRVNH 434

```

```

RESULT 9
US-11-246-999-43
; Sequence 43, Application US/11246999
; Publication No. US20060099622a1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-246-999-43

```

```

Query Match      5.5%; Score 192.5; DB 7; Length 1034;
Best Local Similarity 30.1%; Pred. No. 9.8e-06;
Matches 65; Conservative 31; Mismatches 89; Indels 31; Gaps 8;
Qy      453 TNGFVSLHVOVSGHHTKLOPLVRCVDTDLRLACSKTCLNSADIGFVIDSSSVGTGNFR 512
      135 TTGMCS--RVNSNFPKSKVVALQR-----CQYMDIVIVLDGNSIYP--WV 179
Qy      513 TVLOFTNLTKFEPISTDRIGAVOYTYEORLEFGFDKYSKPDILNAIKRGVWSGST 572
      180 EVGHFLINILKKFTIIGRQIQVGVYGEDVHFEHLNDYSVDVDEASHID--RGCT 238
Qy      573 STGAA--INFALQLFK--SKPNKKMLMLITDGRSYD--DVRIPAMAHLKGVITTAIG 627
      239 ERTTAFGLIEFARSAFQKGRKAKVMIVITDGHSDSPLEKVIQOSERDNTTRYAVA 298
Qy      628 VAW-----AAOEELVIAHPARHSEFFVDE 653
Db      299 VLGYNRRGINPETFLEIKYIASDPDKHFFNVTD 334

```

```

RESULT 10
US-11-246-999-35
; Sequence 35, Application US/11246999
; Publication No. US20060099622a1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407

```

```

; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 35
; LENGTH: 1189
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-11-246-999-35
```

```

Query Match 5.5%; Score 192.5; DB 7; Length 1189;
Best Local Similarity 30.1%; Pred. No. 1.2e-05;
Matches 65; Conservative 31; Mismatches 89; Indels 31; Gaps 8;
```

```

QY 453 TNGFYSLHVQSWFGLHKLTPLVKRVCDTDLRLACSKTCLNSADIGFVIDGSSSVGTGNFR 512
DB 135 TTGMCS-RVNSNFRFSKTVA PALOR-----CQTYMDIVIVLDGNSIYP--WV 179
QY 513 TVLQFTNLTKPEISDTDRIGAVQYTYEORLEFGFDKYSKPDILNAIKRVGVMGCT 572
DB 180 EVQHFLINILKKEYIGGQIQVGVOYGEDVHFEHLNDRSVKDVVEASHIEQ-RGGT 238
QY 573 STGAA--INFALQOLFVK-SKPNRKLMLITDGRSYD--DVRIPAMAHLKGVITYAIG 627
DB 239 ETTATGIEFARSAFQKGRKAKKMYITTDGSHSDPLEKVIQOQSERDNTRYAVA 298
QY 628 VAM-----AAOELEVIATHPARHSFFVDE 653
DB 299 VLGYYNRGINPETFLNEIKYIASDPDDKHFENVTD 334
```

```

RESULT 11
US-11-293-697-3386
; Sequence 3386, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 3458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3386
; LENGTH: 437
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-11-293-697-3386
```

```

Query Match 5.4%; Score 190.5; DB 7; Length 437;
Best Local Similarity 30.1%; Pred. No. 3.9e-06;
Matches 65; Conservative 30; Mismatches 90; Indels 31; Gaps 8;
```

```

QY 453 TNGFYSLHVQSWFGLHKLTPLVKRVCDTDLRLACSKTCLNSADIGFVIDGSSSVGTGNFR 512
DB 135 TTGMCS-RVNSNFRFSKTVA PALOR-----CQTYMDIVIVLDGNSIYP--WV 179
QY 513 TVLQFTNLTKPEISDTDRIGAVQYTYEORLEFGFDKYSKPDILNAIKRVGVMGCT 572
DB 180 EVQHFLINILKKEYIGGQIQVGVOYGEDVHFEHLNDRSVKDVVEASHIEQ-RGGT 238
QY 573 STGAA--INFALQOLFVK-SKPNRKLMLITDGRSYD--DVRIPAMAHLKGVITYAIG 627
DB 239 ETTATGIEFARSAFQKGRKAKKMYITTDGSHSDPLEKVIQOQSERDNTRYAVA 298
QY 628 VAM-----AAOELEVIATHPARHSFFVDE 653
DB 299 VLGYYNRGINPETFLNEIKYIASDPDDKHFENVTD 334
```

```

RESULT 12
US-09-970-076-4
; Sequence 4, Application US/09970076
; Publication No. US20060110801A1
; GENERAL INFORMATION:
; APPLICANT: Young, John A.T.
; APPLICANT: Bradley, Kenneth A.
; APPLICANT: Collier, Robert J.
; APPLICANT: Mogridge, Jeremy S.
; TITLE OF INVENTION: Antitoxin Receptor
; FILE REFERENCE: 960296,97745
; CURRENT APPLICATION NUMBER: US/09/970,076
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/251,481
; PRIOR FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 198
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-09-970-076-4
```

```

Query Match 4.9%; Score 170.5; DB 1; Length 198;
Best Local Similarity 36.8%; Pred. No. 3e-05;
Matches 42; Conservative 18; Mismatches 51; Indels 3; Gaps 2;
```

```

QY 292 IDSFLIDGSTSGKRRFRIOQLADVAQALDIGRGLMGVGVGDNPATHTFNLTHT 351
DB 5 IDVVVVCDESNST--YPMVAVKNFLEKFFVQGLDIGTKTQVGLIOYANRRVVFNLTATYK 62
QY 352 NSRDLKTAIEKIRORG-SLVNVRALSFVTKNFFSKANGRSAGPNNVVVVMDG 404
DB 63 TKEMVATSTQTSQYGEDLTNTFGALQYARKKAYSAGGRSAAATKVMVVTDG 116
```

```

RESULT 13
US-10-196-749-70
; Sequence 70, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gueney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
```

```
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See file wrapper or PALM.
; SEQ ID NO 70
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-70

Query Match          4.1%; Score 143.5; DB 6; Length 500;
Best Local Similarity 34.9%; Pred. No. 0.0085;
Matches 38; Conservative 15; Mismatches 43; Indels 13; Gaps 4;

QY      29  ETAKKIRPKFTVPOINCDVAKGIID-----PEFIVKCPAGCQ--DPKY-HVYGTGTD 77
      379  QSANSFTVSKVTVOAVTCETVEDLCPHKPASHCPR--VYCPNQCWQANPHYARVIGTR 436
DB
QY      78  VYASYSVCCAAVHSGVLDSGSKILVRKAVAGSGSYKSGSYNGVQSL 126
      437  VYSDLSISICRAAVHAGVVRNHHGGYDVPVDRKRTYIASFQNGIFSESL 485
DB

RESULT 14
US-11-293-697-3442
; Sequence 3442, Application US/11293697
; Publication No. US20060105376m1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NOVEL full length CDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3442
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3442

Query Match          3.8%; Score 133.5; DB 7; Length 524;
Best Local Similarity 38.6%; Pred. No. 0.045;
Matches 32; Conservative 14; Mismatches 34; Indels 3; Gaps 2;

QY      44  INCVDVAKGIIDPEFIVKCPAGCQDPKYHYVG--TDVYASYSVCCAAVHSGVL-DNSGG 100
      156  ITCLEASHYKTYEYKFCPCAGCRDVAAGDISGNMWDGYRDTSLCKAIIHAGIADDELGG 215
DB
QY      101  KILVRKAVAGSGSYKSGSYNGVQSL 123
      216  QISVLQRKGIISRYEGIIANGVLS 238
DB

RESULT 15
US-11-330-353-4
; Sequence 4, Application US/11330353
; Publication No. US20060105429m1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
```

```
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/330,353
; FILING DATE: 12-Jan-2006
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,624
; FILING DATE: 10-Sep-2002
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-Jan-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-Jul-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-Jan-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-Jan-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith P.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-330-353-4

Query Match          3.8%; Score 131.5; DB 7; Length 247;
Best Local Similarity 23.3%; Pred. No. 0.021;
Matches 44; Conservative 34; Mismatches 100; Indels 11; Gaps 6;

QY      490  CINSADIGFVIDSSSVGTGNFRTVLQFVNLTKFEISDTDRIGAVQYTYEQRLEFGF 549
      43  CSRLLDLVFLDDSSSRLEAEFEVLKAFVDMERLRIISQKVAVAVEYHDSHAYIGL 102
DB
QY      550  DKYSKPDILNAIKRVGWSGG--TSTGAALNPLLEQFFK-SKPNRKMLITTDGR-- 604
      103  -KDRKRPESELRIASQKVAGSGVASTSEVLYKTLFOIFSKIDRPEASRIALLMASQEP 161
DB
QY      605  ---SYDDVRIPAMAHLKGVITTAIVA--WAAQSELEVIATHPARDHSFPVDEFDNIHQY 660
      162  QRMSRNFVRY-VQGLKKKKVIVIPVGIGPHANLKQIRLIKQAPENKAFVLSVDELEQQ 220
DB
QY      661  VPRITQNIC 669
      221  RDEIVSYLC 229
DB

Search completed: June 7, 2006, 01:35:10
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OM protein - protein search, using sw model

Run on: June 7, 2006, 01:38:52 ; Search time 44 Seconds
(without alignments)
1482.613 Million cell updates/sec

Title: US-10-063-540-34

Perfect score: 678
Sequence: 1 MRTVVLTKASVIEMLVL.....QVPRITQICTEFNQPRN 678

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

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Post-processing: Listing first 45 summaries

Database :

1: PIR_80:.*
2: pir1:.*
3: pir2:.*
4: pir3:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Query Length | DB ID | Description |
|------------|-------|-------------|--------------|----------|--------------------|
| 1 | 8 | 1.2 | 174 | 2 D87197 | conserved hypotet |
| 2 | 8 | 1.2 | 230 | 2 H95040 | hypothetical prote |
| 3 | 8 | 1.2 | 323 | 1 H64130 | glycosyl transfera |
| 4 | 8 | 1.2 | 359 | 2 T44816 | btp protein (impor |
| 5 | 8 | 1.2 | 368 | 2 F84300 | bacteriorhodopsin |
| 6 | 8 | 1.2 | 394 | 2 A97244 | moaA/NirX family F |
| 7 | 8 | 1.2 | 400 | 1 J00756 | nicotinate phospho |
| 8 | 8 | 1.2 | 400 | 2 F90755 | nicotinate phospho |
| 9 | 8 | 1.2 | 400 | 2 D85619 | nicotinate phospho |
| 10 | 8 | 1.2 | 452 | 2 AG1223 | cobyrinic acid a,c |
| 11 | 8 | 1.2 | 695 | 2 C86731 | copper-potassium t |
| 12 | 8 | 1.2 | 1464 | 2 T13716 | bazooka gene prote |
| 13 | 8 | 1.0 | 40 | 2 S08656 | protein VI - human |
| 14 | 8 | 1.0 | 45 | 2 A45700 | envelope glycoprot |
| 15 | 8 | 1.0 | 96 | 2 T11096 | NMDH2 dehydrogenas |
| 16 | 8 | 1.0 | 107 | 2 T19221 | hypothetical prote |
| 17 | 8 | 1.0 | 115 | 2 S38715 | Ig kappa chain V r |
| 18 | 8 | 1.0 | 129 | 2 B64510 | hypothetical prote |
| 19 | 8 | 1.0 | 131 | 2 C82462 | hypothetical prote |
| 20 | 8 | 1.0 | 137 | 2 T06380 | histone H2B-3 - to |
| 21 | 8 | 1.0 | 141 | 2 T48925 | ribosomal L1 prote |
| 22 | 8 | 1.0 | 147 | 2 T09722 | histone H2B1 - upl |
| 23 | 8 | 1.0 | 152 | 2 S48838 | histone H2B - gard |
| 24 | 8 | 1.0 | 153 | 2 F95336 | hypothetical prote |
| 25 | 8 | 1.0 | 156 | 1 GNVOL2 | genome-linked prot |
| 26 | 8 | 1.0 | 156 | 1 GNVOL2 | genome-linked prot |
| 27 | 8 | 1.0 | 156 | 1 GNVOL2 | genome-linked prot |
| 28 | 8 | 1.0 | 172 | 2 F84383 | hypothetical prote |
| 29 | 8 | 1.0 | 172 | 2 C64400 | hypothetical prote |

| | | | | | |
|----|---|-----|-----|----------|--------------------|
| 30 | 7 | 1.0 | 177 | 2 G64071 | H--transporting tw |
| 31 | 7 | 1.0 | 217 | 1 J50630 | formate dehydrogen |
| 32 | 7 | 1.0 | 217 | 2 H90888 | formate dehydrogen |
| 33 | 7 | 1.0 | 217 | 2 A85729 | formate dehydrogen |
| 34 | 7 | 1.0 | 235 | 2 A36941 | phosphoribosylamin |
| 35 | 7 | 1.0 | 235 | 2 H95004 | hypothetical prote |
| 36 | 7 | 1.0 | 236 | 1 A30225 | regulatory protein |
| 37 | 7 | 1.0 | 37 | 2 T51073 | regulatory protein |
| 38 | 7 | 1.0 | 243 | 2 H95282 | probable lysR-type |
| 39 | 7 | 1.0 | 249 | 2 E97877 | phosphoribosylamin |
| 40 | 7 | 1.0 | 256 | 2 AD2307 | hypothetical prote |
| 41 | 7 | 1.0 | 257 | 2 G70581 | hypothetical prote |
| 42 | 7 | 1.0 | 258 | 2 UQ1666 | transcription init |
| 43 | 7 | 1.0 | 261 | 2 C72488 | probable indole-3- |
| 44 | 7 | 1.0 | 267 | 2 AB1280 | probable sigma fac |
| 45 | 7 | 1.0 | 268 | 2 B75279 | survival protein S |

ALIGNMENTS

RESULT 1

D87197 conserved hypothetical protein ML2304 [imported] - Mycobacterium leprae

C/Species: Mycobacterium leprae

C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 31-Dec-2004

C/Accession: D87197

R/Cole, S.T.; Bigmiller, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Dutroy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squ

A/Title: Massive gene decay in the leprosy bacillus.

A/Reference number: A86909; MUID:21128732; PMID:11234002

A/Accession: D87197

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-174 <STO>

A/Cross-references: UNIPROT:Q9CB89; UNIPARC:UPI00000C6E68; GB:AL450380; NID:g13093929; P

C/Genetics:

A/Gene: ML2304

C/Superfamily: translation initiation inhibitor. TrcF type

Query Match 1.2%; Score 8; DB 2; Length 174;

Best Local Similarity 100.0%; Pred.No.7.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 VGADVSIG 268

Db 76 VGADVSIG 83

RESULT 2

H95040 hypothetical protein SP0348 [imported] - Streptococcus pneumoniae (strain TIGR4)

C/Species: Streptococcus pneumoniae

C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C/Accession: H95040

R/Tetelid, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

son, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, W.R.; Radune, D.; Holtzapfle,

nson, T.; Hickey, E.R.; Holt, I.E.

Science 293, 498-506, 2001

A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A/Reference number: A95000; MUID:21357209; PMID:11463916

A/Accession: H95040

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-230 <KUR>

A/Cross-references: UNIPROT:Q97S16; UNIPARC:UPI0000128247; GB:AE005672; PIDN:AAK74521.1;

A/Experimental source: strain TIGR4

C/Genetics:

A/Gene: SP0348

C:Superfamily: Streptococcus agalactiae cpsB protein

Query Match 1.2%; Score 8; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 593 KRKLMI 600
|||||
DB 20 KRKLMI 27

RESULT 3

H64130
glycosyl transferase homolog H1578 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: H64130

R:Plaschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: H64130

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1333 <RIGR>
A:Cross-references: UNIPROT:Q57287; UNIPARC:UPI000013AD7D; GB:U32832; GB:L42023; NID:915
C:Superfamily: Neisseria meningitidis glycosyl transferase A

Query Match 1.2%; Score 8; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ETAKIKR 36
|||||
DB 231 ETAKIKR 238

RESULT 4

T44816
bfp protein [imported] - Halobacterium salinarum

C:Species: Halobacterium salinarum

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T44816

R:Beilach, M.; Friedman, J.; Boyer, H.W.; Pfeiffer, F. Nucleic Acids Res. 12, 7949-7959, 1984
A:Title: Characterization of a halobacterial gene affecting bacterio-opsin gene expression
A:Reference number: Z22850; MUID:85037955; PMID:6093059

A:Accession: T44816

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-359 <BST>

A:Cross-references: UNIPROT:Q47973; UNIPARC:UPI00000628C3; EMBL:X01081; PIDD:CAA25558.1
A:Note: the source is designated as Halobacterium halobium
C:Genetics:

A:Gene: bfp

Query Match 1.2%; Score 8; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 LAVTAVA 195
|||||
DB 111 LAVTAVA 118

RESULT 5

F84300
bacteriorhodopsin related protein [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: F84300

R:Ng, W.V.; Kennedy, S.P.; Mahafiras, G.G.; Bergiet, B.; Pan, M.; Shukla, H.D.; Laeky, S.; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li, A.; Title: Genome sequence of Halobacterium species NRC-1. A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: F84300

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-368 <STO>

A:Cross-references: UNIPROT:Q9HPU7; UNIPARC:UPI00000638C8; GB:AE004437; NID:910580962, P3
C:Genetics:

A:Gene: bfp

Query Match 1.2%; Score 8; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 188 LAVTAVA 195
|||||
DB 120 LAVTAVA 127

RESULT 6

A97244
moa/NirX family Fe-S oxidoreductase CAC2796 [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C:Accession: A97244

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: A97244

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-394 <KUR>

A:Cross-references: UNIPROT:Q97FE3; UNIPARC:UPI000006CA53; GB:AE001437; PIDD:AAK80740.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:

A:Gene: CAC2796

Query Match 1.2%; Score 8; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 KETAKIK 35
|||||
DB 125 KETAKIK 132

RESULT 7

JQ0756
nicotinate phosphoribosyltransferase (EC 2.4.2.11) - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: JQ0756; B64833

R:Whitbolts, M.G.; Terpestra, P.; van Belien, J.B.; Kingma, J.; Meester, H.A.R.; Witholt, J. Biol. Chem. 265, 17665-17672, 1990
A:Title: Variation of cofactor levels in Escherichia coli; sequence analysis and expression

A:Reference number: JQ0756; MUID:91009224; PMID:2211655

A:Accession: JQ0756

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-400 <WUB>

A:Cross-references: UNIPROT:P18133; UNIPARC:UPI0000168062; GB:J05568; NID:9147306; PIDD:J
A:Experimental source: strain GEC70
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of *Escherichia coli* K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: B64833
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-400 <BLAT>
A/Cross-references: UNIPARC:UPI0000168062; GB:AE000195; GB:U00096; NID:g1787156; PIDN:AA
A/Experimental source: strain K-12, substrain MG1655
C/Genetics:
A:Gene: pncB
C/Function:
A/Pathway: nicotinate and nicotinamide metabolism
C/Superfamily: nicotinate phosphoribosyltransferase
C/Keywords: glycosyltransferase; pentosyltransferase

Query Match 1.2%; Score 8; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 ADVAQAALD 324
DB 141 ADVAQAALD 148

RESULT 8
F90755
nicotinate phosphoribosyltransferase [imported] - *Escherichia coli* (strain O157:H7, sube
C/Species: *Escherichia coli*
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: F90755
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genc
A/Reference number: A95629; MUID:21156231; PMID:1158796
A/Accession: F90755
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-400 <NAV>
A/Cross-references: UNIPROT:Q8YDE8; UNIPARC:UPI00001653E6; GB:BA000007; PIDN:BA834437.1;
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A:Gene: Ecs1014
C/Superfamily: nicotinate phosphoribosyltransferase

Query Match 1.2%; Score 8; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 ADVAQAALD 324
DB 141 ADVAQAALD 148

RESULT 9
D85619
nicotinate phosphoribosyltransferase [imported] - *Escherichia coli* (strain O157:H7, sube
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: D85619
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobbeck, E.J.; Davis, N.W.; Llim, A.; Dimalanta, E.; Potamotis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: D85619
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-400 <STO>
A/Cross-references: UNIPROT:Q8YDE8; UNIPARC:UPI00001653E6; GB:AE005174; NID:g12514106; F
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A:Gene: pncB

C/Superfamily: nicotinate phosphoribosyltransferase

Query Match 1.2%; Score 8; DB 2; Length 400;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 ADVAQAALD 324
DB 141 ADVAQAALD 148

RESULT 10
AG1223
cobyrrinic acid a,c-diamide synthase homolog *chlA* [imported] - *Listeria monocytogenes* (st
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AG1223
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Biocker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fsihl, H.
Science 294, 849-852, 2001
D.; Jones, L.M.; Karac, U.
A/Authors: Kretz, U.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlutener, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A/Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AG1223
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-452 <GLA>
A/Cross-references: UNIPROT:Q8Y7T0; UNIPARC:UPI0000054E4C; GB:NC_003210; PIDN:CAC99269.1
A/Experimental source: strain EGD-e
C/Genetics:
A:Gene: *chlA*
C/Superfamily: cobyrinic acid a,c-diamide synthase

Query Match 1.2%; Score 8; DB 2; Length 452;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 267 LGVLPKEE 274
DB 191 LGVLPKEE 198

RESULT 11
C86731
copper-potassium transporting ATPase B *copB* [imported] - *Lactococcus lactis* subsp. *lacti*
C/Species: *Lactococcus lactis* subsp. *lactis*
C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C/Accession: C86731
R/Bolotin, A.; Winkler, P.; Manger, S.; Jallou, O.; Malame, K.; Weissenbach, J.; Ehrlich,
Genome Res. 11, 731-753, 2001
A/Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp
A/Reference number: A86625; MUID:21235186; PMID:11137471
A/Accession: C86731
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-695 <STO>
A/Cross-references: UNIPROT:Q9CH87; UNIPARC:UPI000000C919; GB:AE005176; PID:g12723778; P
A/Experimental source: strain IL1403
C/Genetics:
A:Gene: *copB*
C/Superfamily: Enterococcus copper-transporting ATPase *copB*; ATPase nucleotide-binding dc

Query Match 1.2%; Score 8; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 NKETAKKI 34
DB 540 NKETAKKI 547

RESULT 12

T11716
bazooka gene protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C/Accession: T11716
R/Kuchinke, U.; Grawe, F.; Knust, E.
Submitted to the EMBL Data Library, November 1998
A/Description: Control of spindle orientation in Drosophila by the Par-3-related PDZ-dom
A/Reference number: Z17708
A/Accession: T11716
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1464 <KUC>
A/Cross-references: UNIPROT:O96782; UNIPARC:UPI0000079EAF; EMBL:AJ130871; NID:e1363519;
C/Genetics:
A:Gene: bazooka
A/Cross-references: FlyBase:FBgn0000163
A/Map position: X

Query Match
Best Local Similarity 100.0%; DB 2; Length 1464;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 502 GSSSVGTG 509
Db 96 GSSSVGTG 103

RESULT 13

S08656
protein VI - human adenovirus 41 (fragment)
C:Species: Mastadenovirus h41 (human adenovirus 41)
A/Note: host Homo sapiens (man)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: S08656
R/Toogood, C.I.A.; Murali, R.; Burnett, M.; Hay, R.T.
Submitted to the EMBL Data Library, February 1990
A/Reference number: S08656
A/Accession: S08656
A/Molecule type: DNA
A/Residues: 1-40 <TOO>
A/Cross-references: UNIPROT:P16139; UNIPARC:UPI0000170DA4; EMBL:X51783; NID:G58562; PIDN:
C/Superfamily: adenovirus polypeptide VI

Query Match
Best Local Similarity 100.0%; DB 2; Length 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 191 TVAVATP 197
Db 4 TVAVATP 10

RESULT 14

A45700
envelope glycoprotein E2 (hypervariable region, variant clone M.1) - hepatitis C virus
C:Species: hepatitis C virus
C>Date: 16-Feb-1994 #sequence_revision 16-Nov-1994 #text_change 09-Jul-2004
C/Accession: A45700
R/Weiner, A.J.; Thaler, M.M.; Crawford, K.; Ching, K.; Kansopon, J.; Chien, D.Y.; Hall, J.
J. Virol. 67, 4365-4368, 1993
A/Title: A unique, predominant hepatitis C virus variant found in an infant born to a mc
A/Reference number: A45700; MUID:93287257; PMID:8389933
A/Accession: A45700
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-45 <WEI>
A/Cross-references: UNIPROT:Q86615; UNIPARC:UPI00000F7881; GB:S62395; NID:G386130; PIDN:
A/Experimental source: non-human immunodeficiency virus type 1-infected mother
A/Note: sequence extracted from NCBI backbone (NCBIN:133708, NCBIPI:133709)
C/Superfamily: hepatitis C virus genome polyprotein
C/Keywords: glycoprotein

Query Match
Best Local Similarity 100.0%; DB 2; Length 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 206 SAASTTS 212
Db 22 SAASTTS 28

RESULT 15

T11096
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - Dinodon semicarinatus mitochondr
C:Species: mitochondrion Dinodon semicarinatus
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T11096
R/Kumazawa, Y.; Ota, H.; Nishida, M.; Ozawa, T.
Genetics 150, 313-329, 1998
A/Title: The complete nucleotide sequence of a snake (Dinodon semicarinatus) mitochondri
A/Reference number: Z17247; MUID:98393589; PMID:9725849
A/Accession: T11096
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-96 <KUM>
A/Cross-references: UNIPROT:O79554; UNIPARC:UPI0000130990; EMBL:AB008539; PIDN:BAJ33030.1
A/Experimental source: liver
C/Genetics:
A:Genome: mitochondrion
C/Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C/Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation; c

Query Match
Best Local Similarity 100.0%; DB 2; Length 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 SVCGAAV 90
Db 67 SVCGAAV 73

Search completed: June 7, 2006, 01:44:33
Job time : 46 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 7, 2006, 01:35:23 ; Search time 304 Seconds
(without alignments)
2063.028 Million cell updates/sec

Title: US-10-063-540-34

Perfect score: 678
Sequence: 1 MRTVLTLMKASVIEMLVL.....QYVPRITICTEFNSQPRN 678

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 6

Total number of hits satisfying chosen parameters: 28349

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Uniprot_7.2.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------|
| 1 | 678 | 100.0 | 678 | 2 | Q6UX17_HUMAN |
| 2 | 411 | 60.6 | 693 | 2 | Q9UND0_HUMAN |
| 3 | 259 | 38.2 | 656 | 2 | Q96DPT_HUMAN |
| 4 | 163 | 24.0 | 203 | 2 | Q6P7T3_HUMAN |
| 5 | 58 | 8.6 | 650 | 2 | Q3T247_MOUSE |
| 6 | 45 | 8.4 | 652 | 2 | Q95L12_BOVIN |
| 7 | 45 | 6.6 | 628 | 2 | Q8BQ41_MOUSE |
| 8 | 45 | 6.6 | 650 | 2 | Q8K047_MOUSE |
| 9 | 45 | 6.6 | 650 | 2 | Q8VH15_MOUSE |
| 10 | 45 | 6.6 | 650 | 2 | Q9C7Z1_MOUSE |
| 11 | 23 | 3.7 | 680 | 2 | Q4RP27_TETNG |
| 12 | 23 | 3.4 | 748 | 2 | Q5NTW9_CHICK |
| 13 | 11 | 1.6 | 553 | 2 | Q8AM56_BRARE |
| 14 | 10 | 1.5 | 1070 | 2 | Q4N1B8_THERP |
| 15 | 10 | 1.5 | 1197 | 2 | Q4URP9_THERN |
| 16 | 9 | 1.3 | 347 | 2 | Q2T7S9_BURTH |
| 17 | 9 | 1.3 | 347 | 2 | Q3JK55_BURP1 |
| 18 | 9 | 1.3 | 347 | 2 | Q63JB1_BURP5 |
| 19 | 9 | 1.3 | 387 | 2 | Q4JVA3_CORUK |
| 20 | 9 | 1.3 | 560 | 2 | Q4C273_CROWT |
| 21 | 9 | 1.3 | 598 | 2 | Q6G3F2_BAARH |
| 22 | 8 | 1.2 | 63 | 2 | Q4YMI5_PLAAB |
| 23 | 8 | 1.2 | 100 | 2 | Q7G2C1_ORYSA |
| 24 | 8 | 1.2 | 106 | 2 | Q4KKH3_PSEFS |
| 25 | 8 | 1.2 | 112 | 2 | Q8G578_BIFLO |
| 26 | 8 | 1.2 | 117 | 2 | Q47M29_THERF |
| 27 | 8 | 1.2 | 124 | 2 | Q480F6_COLP3 |
| 28 | 8 | 1.2 | 155 | 2 | Q7BUZ6_STRPN |
| 29 | 8 | 1.2 | 173 | 2 | Q4SDS4_TETNG |
| 30 | 8 | 1.2 | 174 | 2 | Q9CB89_MYCLE |
| 31 | 8 | 1.2 | 180 | 2 | Q2T220_BURTH |

| | | | | | | |
|----|---|-----|-----|---|--------------|--------------------|
| 32 | 8 | 1.2 | 208 | 2 | Q4U442_THERN | Q4U442 theileria a |
| 33 | 8 | 1.2 | 208 | 2 | Q21MA3_RHOA | Q21ma3 rhodopseudo |
| 34 | 8 | 1.2 | 208 | 2 | Q66166_BRARE | Q66166 brachydanio |
| 35 | 8 | 1.2 | 208 | 2 | Q90Z99_BRARE | Q90z99 brachydanio |
| 36 | 8 | 1.2 | 211 | 2 | Q4N6H5_THERP | Q4n6h5 theileria p |
| 37 | 8 | 1.2 | 217 | 2 | Q3GE72_SYTRM | Q3ge72 syntrophomo |
| 38 | 8 | 1.2 | 230 | 1 | QPSCI1_STRPN | Qpsci1 streptococc |
| 39 | 8 | 1.2 | 230 | 2 | Q546S7_STRPN | Q546s7 streptococc |
| 40 | 8 | 1.2 | 230 | 2 | Q7BV01_STRPN | Q7bv01 streptococc |
| 41 | 8 | 1.2 | 230 | 2 | Q8KM01_STRPN | Q8km01 streptococc |
| 42 | 8 | 1.2 | 231 | 2 | Q868S7_STRPN | Q868s7 streptococc |
| 43 | 8 | 1.2 | 231 | 2 | Q371R7_RHOA | Q371r7 rhodopseudo |
| 44 | 8 | 1.2 | 231 | 2 | Q4JYK9_STRPN | Q4jyk9 streptococc |
| 45 | 8 | 1.2 | 231 | 2 | Q4JYPO_STRPN | Q4jypo streptococc |

ALIGNMENTS

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RESULT 1
06UX17_HUMAN PRELIMINARY; PRT; 678 AA.
ID Q6UX17_HUMAN
AC Q6UX17
DT 24-MAY-2005, integrated into UniprotKB/TREMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE VIT.
GN ORFNames=UNO647;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Eason D., Foster J.S., Grimaldi C., Gu O., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Kimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simons L., Singh V., Smith V., Stinson J., Vagts A.,
RA Vanden R.L., Matanabe C., Wleand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SDPI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
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EMBL: AY358338; AAC88704.1; -, mRNA.
DR HSSP; Q43405; IJBI.
DR InterPro; IPR004043; LCCL.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VWA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWF_A; 2.
DR PROSITE; PS50234; VWF_A; 2.
SQ SEQUENCE 678 AA; 73930 MW; 9870E75A218C686C CRC64;

Query Match 100.0%; Score 678; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTLMKASVIEMLVLIVTGVSNKETAKIKREKFTVPQINCVDKAGKITDPEFIV 60
DB 1 MRTVLTLMKASVIEMLVLIVTGVSNKETAKIKREKFTVPQINCVDKAGKITDPEFIV 60
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QY 61 KCPAGCDDPKHYVGTDVYASYSVCGAAVHSGVLDNSGKILVRKYGAGSGYKGSNG 120
 DB 61 KCPAGCDDPKHYVGTDVYASYSVCGAAVHSGVLDNSGKILVRKYGAGSGYKGSNG 120
 QY 121 VQSLPRMRESFVLESKPKKGYTPSALTYSSSKAPAAAGETTAYORPPIPGTTAQ 180
 DB 121 VQSLPRMRESFVLESKPKKGYTPSALTYSSSKAPAAAGETTAYORPPIPGTTAQ 180
 QY 181 PVTLMQLLATVAVATPTTLPRPSPASASTTSTRPOSVGRSDEMMLSTATYTSSQNR 240
 DB 181 PVTLMQLLATVAVATPTTLPRPSPASASTTSTRPOSVGRSDEMMLSTATYTSSQNR 240
 QY 241 PRADPGIQRDDPSGAFOKPGVAGVSLGLVPEKELSTQSLPVLGDPNCKIDSLFILDG 300
 DB 241 PRADPGIQRDDPSGAFOKPGVAGVSLGLVPEKELSTQSLPVLGDPNCKIDSLFILDG 300
 QY 301 STSIGKRFRIOQLADVAQALDIGAPGLMGVVOYGDNPATHPNLKTHNSRDLXTAI 360
 DB 301 STSIGKRFRIOQLADVAQALDIGAPGLMGVVOYGDNPATHPNLKTHNSRDLXTAI 360
 QY 361 EKTTRGGLSNVGRALSFVTKNFSSKANGNSGAPNVVVVWDGMPDKVEASRLARES 420
 DB 361 EKTTRGGLSNVGRALSFVTKNFSSKANGNSGAPNVVVVWDGMPDKVEASRLARES 420
 QY 421 GINIFFTIEGAANEKQYVEPNFANKAVCRITNGFSLHVQSFGLHKTLOPLVKEVCD 480
 DB 421 GINIFFTIEGAANEKQYVEPNFANKAVCRITNGFSLHVQSFGLHKTLOPLVKEVCD 480
 QY 481 TDRACSKTCLNSADIFVIDGSSVGTGNFRVLOFVTNLTKPEFISDTRIGAVOYT 540
 DB 481 TDRACSKTCLNSADIFVIDGSSVGTGNFRVLOFVTNLTKPEFISDTRIGAVOYT 540
 QY 541 YERLEGFPGYSSKPIILNAIKVWGSGTSGAIPALBQLFKSKPKKMKMILI 600
 DB 541 YERLEGFPGYSSKPIILNAIKVWGSGTSGAIPALBQLFKSKPKKMKMILI 600
 QY 601 TDRSYDVDAIPMAAHLKGVITVIAIGVAMAQEBELVIAITHPADHSFVDEFDNLHOY 660
 DB 601 TDRSYDVDAIPMAAHLKGVITVIAIGVAMAQEBELVIAITHPADHSFVDEFDNLHOY 660
 QY 661 VPRIIQNICTEFNSQPRN 678
 DB 661 VPRIIQNICTEFNSQPRN 678

RESULT 2
 Q9UDNO_HUMAN PREDIMINARY; PRT; 693 AA.
 ID Q9UDNO_HUMAN PREDIMINARY; PRT; 693 AA.
 AC Q9UDNO; Q96DM8;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 2.
 DT 07-MAR-2006, entry version 26.
 DE Hypothetical protein VIT (Hypothetical protein FLJ32210).
 GN Name=VIT;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Cordes M., Kalicki J., Ames M.,
 RT "The sequence of Homo sapiens BAC clone RP11-294111."
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.H.,
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Waterston R.,
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Wilson R.K.,
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura T., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yaeda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosioki T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Niimura K., Iehibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimura M., Watanabe M., Hirataka S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano Y.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
 RA Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Masegawa K., Yumiki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshihawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Teraishiima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Taehiro H., Tanigami A., Fujitaya T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohnori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
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 CC
 DR EMBL; AK056772; BAB71279.1; -; mRNA.
 DR EMBL; AC007363; AAF19243.2; -; Genomic_DNA.
 DR HSSP; O43405; 1JBT.
 DR HGNC; HGNC:12697; VIT.
 DR InterPro; IPR004043; LCCL.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF03815; LCCL; 1.
 DR Pfam; PF00092; VMA; 2.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00603; LCCL; 1.
 DR SMART; SM00327; VMA; 2.
 DR PROSITE; PS50820; LCCL; 1.
 DR PROSITE; PS50234; VMPA; 2.
 KM Hypothetical protein.
 SQ SEQUENCE 693 AA; 75575 MW; 2DB8B2421F2D496D CRC64;

Query Match 60.6%; Score 411; DB 2; Length 693;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 268 GLVPEKELSTQSLPVLGDPNCKIDSLFIDSGTSGIKRRFRIOQLADVAQALDIGP 327
 DB 268 GLVPEKELSTQSLPVLGDPNCKIDSLFIDSGTSGIKRRFRIOQLADVAQALDIGP 342
 QY 328 AGPLMGVVOYGDNPATHPNLKTHNSRDLXTALEKTTRGGLSNVGRALSFVTKNFSSKA 387
 DB 343 AGPLMGVVOYGDNPATHPNLKTHNSRDLXTALEKTTRGGLSNVGRALSFVTKNFSSKA 402
 QY 388 NGRSGAPNVVVVWDGMPDKVEASRLAREGINIFFTIEGAANEKQYVEPNFANK 447

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Db 403 NGNSGAPNWWWVWDGWPDTKVEASRLAESGINIFITIEGAENENKQYVVEPNAN 462
Qy 448 KAVERTNGFVSLHVSQWFGHLKHTLOPLVKRYCDPDRCLASCSTCLNSANIGVIOSSSVG 507
Db 463 KAVRTNGFVSLHVSQWFGHLKHTLOPLVKRYCDPDRCLASCSTCLNSAIGVIDSSSVG 522
Qy 508 TGNFRTVLOFTNTLTKFEISDPTDRIGAVOYTYEQRLPEFDFDKSSKPDILNAIKRKY 567
Db 523 TGNFRTVLOFTNTLTKFEISDPTDRIGAVOYTYEQRLPEFDFDKSSKPDILNAIKRKY 582
Qy 568 WSGGTSGAALNPALEBOLFKKSKPNKRKMLITDGRSYDVRIPAMAHLKGVITTAIG 627
Db 583 WSGGTSGAALNPALEBOLFKKSKPNKRKMLITDGRSYDVRIPAMAHLKGVITTAIG 642
Qy 628 VAMAABELEVIATHPARDHSFVDFEFDNLHGYPRRIQNTCTENSGPRN 678
Db 643 VAMAABELEVIATHPARDHSFVDFEFDNLHGYPRRIQNTCTENSGPRN 693

RESULT 3
ID Q96DT1_HUMAN PRELIMINARY; PRT; 656 AA.
AC Q96DT1;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Vitrin.
GN Name=VIT;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal muscle;
RA Ren Z.-X., Liu J.G., Mayne R.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL: AF063833; AAL18263.1; -; mRNA.
DR HSSP: O43405; IJBI.
DR InterPro: IPR004043; LCCL.
DR InterPro: IPR02035; VWF_A.
DR Pfam: PF03815; LCCL; 1.
DR Pfam: PF00092; VMA; 2.
DR PRINTS: PRO0453; VWFADOMAIN.
DR SMART: SM00603; LCCL; 1.
DR SMART: SM00327; VMA; 2.
DR PROSITE: PS50820; LCCL; 1.
DR PROSITE: PS50234; VWF; 2.
SQ SEQUENCE 656 AA; 71768 MW; E242E0DFB07CF2C CRC64;

Query March 38.2%; Score 259; DB 2; Length 656;
Best Local Similarity 100.0%; Pred. No. 6e-257;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 420 SGINIFITIEGAENENKQYVVEPNFANKAVCRITNGFSLHVSQWFGHLKHTLOPLVKRYC 479
Db 398 SGINIFITIEGAENENKQYVVEPNFANKAVCRITNGFSLHVSQWFGHLKHTLOPLVKRYC 457
Qy 480 DTDPLACSKTCLNSADIGFVIDSSSVGTGNFRTVLOFTNTLTKFEISDPTDRIGAVOY 539
Db 458 DTDPLACSKTCLNSADIGFVIDSSSVGTGNFRTVLOFTNTLTKFEISDPTDRIGAVOY 517
Qy 540 TYERLREGFDPKYSKPDILNAIKRKYVWGSSTGALNPALEBOLFKKSKPNKRKMLIT 599
Db 518 TYERLREGFDPKYSKPDILNAIKRKYVWGSSTGALNPALEBOLFKKSKPNKRKMLIT 577
Qy 600 ITDGRSYDVRIPAMAHLKGVITTAIGVAMAABELEVIATHPARDHSFVDFEFDNLHQ 659
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Db 578 ITDGRSYDVRIPAMAHLKGVITTAIGVAMAABELEVIATHPARDHSFVDFEFDNLHQ 637
Qy 660 YVPRRIQNTCTENSGPRN 678
Db 638 YVPRRIQNTCTENSGPRN 656

RESULT 4
ID Q6P7T3_HUMAN PRELIMINARY; PRT; 203 AA.
AC Q6P7T3;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.F., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Umed T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.U., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BC061519; AA61519.1; -; mRNA.
DR InterPro: IPR004043; LCCL.
DR Pfam: PF03815; LCCL; 1.
DR SMART: SM00603; LCCL; 1.
DR PROSITE: PS50820; LCCL; 1.
KV Hypothetical protein.
SQ SEQUENCE 203 AA; 21788 MW; 363B8CF460076BBA CRC64;

Query March 24.0%; Score 163; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.8e-158;
Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTVLLTMKASVLEMPVLVLTGVHSNKETAKKIKRPKFTVPOINCQVKAQGIIDPEFTV 60
Db 1 MRTVLLTMKASVLEMPVLVLTGVHSNKETAKKIKRPKFTVPOINCQVKAQGIIDPEFTV 60
Qy 61 KCPAGCDDPKRYVGTGVYVSYSSVCGAAVHSGVLNDNSGSKILVRYKAQSGYGSYNG 120
Db 61 KCPAGCDDPKRYVGTGVYVSYSSVCGAAVHSGVLNDNSGSKILVRYKAQSGYGSYNG 120
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RC STRAIN=C57BL/6J; TISSUE=inner ear;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shihara K., Itch M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itch M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kasaiwa K.,
RA Fujiwaka Y., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=inner ear;
RA Araiawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Horii F., Iida J., Imanura K., Imotani K., Itch M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shihara K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanaki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR MGI; MGI:1921449; Vlt.
DR GO; GO:0005615; C:extracellular space; RCA.
DR InterPro; IPRO04043; LCCL.
DR InterPro; IPRO02035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWF_A; 2.
DR PROSITE; PS50234; VWF_A; 2.
SQ SEQUENCE 650 AA; 70651 MW; 73D31A1B618C0719 CRC64;

Query Match 8.4%; Score 58; DB 2; Length 650;
Best Local Similarity 100.0%; Pred. No. 7.1e-50;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 VYASYSVCGAAVHSGVLNDSGGKILVRKVAAGSGYKGSYNGVOSLSLPRWRESFV 135
DB 78 VYASYSVCGAAVHSGVLNDSGGKILVRKVAAGSGYKGSYNGVOSLSLPRWRESFV 135

RESULT 6
O95LI2_BOVIN PRELIMINARY; PRT; 652 AA.
AC O95LI2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 2.
DT 07-FEB-2006, entry version 16.
DE Vitrin.
GN Name=VIT;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxId=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RA Ran Z.-X., Liu J.-G., Mayne R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AF063832; AAL18262.2; -; mRNA.

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DR HSSP; O43405; 1UBI.
DR InterPro; IPRO04043; LCCL.
DR InterPro; IPRO02035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; VMA; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VMA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWF_A; 2.
DR PROSITE; PS50234; VWF_A; 2.
SQ SEQUENCE 652 AA; 70873 MW; 3512421CA6987C51 CRC64;

Query Match 8.4%; Score 57; DB 2; Length 652;
Best Local Similarity 100.0%; Pred. No. 7.6e-49;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 77 DVYASYSVCGAAVHSGVLNDSGGKILVRKVAAGSGYKGSYNGVOSLSLPRWRESF 133
DB 77 DVYASYSVCGAAVHSGVLNDSGGKILVRKVAAGSGYKGSYNGVOSLSLPRWRESF 133

RESULT 7
O9BQ41_MOUSE PRELIMINARY; PRT; 628 AA.
AC O9BQ41;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE 12 days embryonic spinal ganglion cDNA. RIKEN full-length enriched
DE library, clone: D130059M21 product: VITRIN homolog.
GN Name=Vlt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritch M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilm M., Zeng L.G., Aldrich S., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aurrealija R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhury V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstler P., Fagioli M., Paulsen G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Guetlich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelich L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Medan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Morteau-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nisason R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sees L., Sheng Y.,
RA Shihara Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,

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RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeai K.,
 RA Yamashita H., Zabarovsky E., Zhu S., Zimmer A., Hilde W., Bult C.,
 RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arikawa T.,
 RA Ikeda J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Maki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.,
 RT "The transcriptional landscape of the mammalian genome.",
 RL Science 309:1559-1563(2005).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RT (Genome Network Core Team) and the FANTOM Consortium;
 RL "Antisense Transcription in the Mammalian Transcriptome.",
 Science 309:1564-1566(2005).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamana K., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schoenbach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochua C., Corbani L.E., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Gaasterland S., Guelincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konecny A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perce G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontus J.U., Qi D., Ramchandran S.,
 RA Ravalet T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sanderlin A., Schneider C., Sempke C.A., Serou M., Shimada K.,
 RA Sultana R., Takemura Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner R., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kikihawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Maki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Schirml F., Suzuki R., Tomita M., Wagner U., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guelincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=204939374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.",
 RL Genome Res. 10:1617-1630(2000).
 [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer.",
 RL Genome Res. 10:1757-1771(2000).
 [8]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akiba S., Takekura Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL: AK051606; BAC34688.1; -- mRNA.
 DR HSPF: O43405; IUBI.
 DR Ensemble: ENSMUSG00000024076; Mus musculus.
 DR MGI: MGI.1921449; Vlt.
 DR GO: GO:0005615; C:extracellular space; RCA.
 DR InterPro: IPR004043; LCCL.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam: PF03815; LCCL; 1.
 DR Pfam: PF00092; VWA; 2.
 DR PRINTS: PR00453; VWFADOMAIN.
 DR SMART: SM00603; LCCL; 1.
 DR SMART: SM00327; VWA; 2.
 DR PROSITE: PSS0820; LCCL; 1.
 DR PROSITE: PSS0234; VWF; 2.
 SQ SEQUENCE 628 AA; 68198 MW; C96C4ACEB9E572480 CRC64;

Query Match 6.6%; Score 45; DB 2; Length 628;
 Best Local Similarity 100.0%; Pred. No. 1; 7e-36;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 HSGVLDNSGGKILVRKVAAGSGYKSGYNSGVGSLSPRWRSEFIV 135
 Db 69 HSGVLDNSGGKILVRKVAAGSGYKSGYNSGVGSLSPRWRSEFIV 113

RESULT 8

Q8K047 MOUSE PRELIMINARY; PRT; 650 AA.
 ID Q8K047 MOUSE PRELIMINARY; PRT; 650 AA.
 AC Q8K047;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Vitrin.
 GN Name=Vlt;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rudin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RA Director MGC Project;
 CC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; BC034120; AAH34120.1; -; mRNA.
 DR HSSP; O43405; IUBI.
 DR Ensembl; ENSMUSG00000024076; Mus musculus.
 DR MGI; MGI:1921449; Vlt.
 DR GO; GO:0005615; C:extracellular space; RCA.
 DR InterPro; IPR004043; LCCL.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF03815; LCCL; 1.
 DR Pfam; PF00092; VMA; 2.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00603; LCCL; 1.
 DR SMART; SM00327; VMA; 2.
 DR PROSITE; PS50820; LCCL; 1.
 DR PROSITE; PS50234; VWF_A; 2.
 SQ SEQUENCE 650 AA; 70699 MW; 1641623E11003B4E CRC64;

Query Match 6.6%; Score 45; DB 2; Length 650;
 Best Local Similarity 100.0%; Pred. No. 1.8e-36;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 HSGVLDSGGKILVRKVAAGSGYSGYSNGVSLPLRMRESFTV 135
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 Db 91 HSGVLDSGGKILVRKVAAGSGYSGYSNGVSLPLRMRESFTV 135

RESULT 9
 Q8VH15_MOUSE

ID Q8VH15_MOUSE PRELIMINARY; PRT; 650 AA.
 AC Q8VH15;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 07-FEB-2006, entry version 17.
 DE Vitrin.
 GN Name=Vlt;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RA Liu J., Ren Z.-X., Takano M., Mayne R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AF454755; AAL57848.1; -; mRNA.
 DR HSSP; O43405; IUBI.
 DR Ensembl; ENSMUSG00000024076; Mus musculus.
 DR MGI; MGI:1921449; Vlt.
 DR GO; GO:0005615; C:extracellular space; RCA.
 DR InterPro; IPR004043; LCCL.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF03815; LCCL; 1.
 DR Pfam; PF00092; VMA; 2.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00603; LCCL; 1.
 DR SMART; SM00327; VMA; 2.
 DR PROSITE; PS50820; LCCL; 1.
 DR PROSITE; PS50234; VWF_A; 2.
 SQ SEQUENCE 650 AA; 70706 MW; FAC0F72APB953940 CRC64;

Query Match 6.6%; Score 45; DB 2; Length 650;
 Best Local Similarity 100.0%; Pred. No. 1.8e-36;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 HSGVLDSGGKILVRKVAAGSGYSGYSNGVSLPLRMRESFTV 135
 |||||
 Db 91 HSGVLDSGGKILVRKVAAGSGYSGYSNGVSLPLRMRESFTV 135

RESULT 10
 Q9CY21_MOUSE PRELIMINARY; PRT; 650 AA.
 ID Q9CY21_MOUSE PRELIMINARY; PRT; 650 AA.
 AC Q9CY21;
 DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2001, sequence version 1.
 DT 07-FEB-2006, entry version 25.
 DE 10-11 days embryo whole body cDNA, RIKEN full-length enriched
 DE library, clone:2810429K11 product:VITRIN, full insert sequence.
 GN Name=Vlt;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=whole body;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=whole body;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Fritsch M.C., Maeda N.,

RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 RA Davis M.J., Wilmng L.G., Aidinis V., Allen J.E.,
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chak A.M.,
 RA Chiu K.P., Choudhary V., Christofels A., Clutterbuck D.R.,
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 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 RA Georgi-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 RA Guetlich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 RA Hall D., Humphreys L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
 RA Jakt M., Knapik A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakanchi H., Ng P.,
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 RA Post B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 RA Schombach C., Sekiguchi K., Sempie C.A., Seno S., Sessa L., Sheng Y.,
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Taki K.,
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yeai K.,
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 RA Gilmann S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
 RA Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Nimomiya N.,
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 RA Tagami M., Waki K., Watabiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
 RA Hayashizaki Y.,
 RT "The transcriptional landscape of the mammalian genome.",
 RL Science 309:1559-1563(2005).
 [3]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.",
 RL Science 309:1564-1566(2005).
 [4]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX PubMed=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Niki K., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Nagai K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,
 RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schmitt L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bird D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Gozlik A., Gough J.,
 RA Gilmann S., Guetlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltas K., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Wetanabe Y., Wells C.,
 RA Wilmng L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Aizawa T., Fukuda S.,
 RA Hara A., Haseizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
 RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.",
 RL Nature 420:563-573(2002).
 [5]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX PubMed=11085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischnann W., Gaasterland T., Giesi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Scudliff F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Maehira J., Mazzarelli J., Monbets P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schombach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilmng L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 [6]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RX PubMed=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer",
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RA NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Whole body;
 RA Adachi J., Aizawa K., Akihara S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hasegawa T., Hara A., Hayatsu N., Hiramoto K., Hiroaka T., Hori F.,
 RA Hoshigaki T., Hara A., Hayatsu N., Hiramoto K., Hiroaka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Koyama S., Kurihara C.,
 RA Kawai J., Kojima Y., Kono H., Kondo M., Koyama S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai K., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toyota T., Yamamura T., Yaunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
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 DR EMBL, AK013193; BAB28702.1; -; mRNA.

DE COCH).
 GN Name=coch; Synonyms=OTDARP0000001491; ORFNames=d2234G15.4-001;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Babbage A.;
 RL Submitted (JBC-2004) to the EMBL/GenBank/DBJ databases.
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 DR EMBL; AL596026; CAD58748.1; -; Genomic_DNA.
 DR HSSP; O43405; 1UBI.
 DR Ensembl; ENSDARG0000024032; Danio rerio.
 DR ZFIN; ZDB-GENE-030616-403; coch.
 DR InterPro; IPR004043; LCCL.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF03815; LCCL; 1.
 DR Pfam; PF00092; VMA; 2.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00603; LCCL; 1.
 DR SMART; SM00327; VMA; 2.
 DR PROSITE; PSS0820; LCCL; 1.
 DR PROSITE; PSS0234; VWF_A; 2.
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Query Match 1.6%; Score 11; DB 2; Length 553;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 293 LARESGINRF 303

RESULT 14
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 ID QAN1B8.THEPA PRELIMINARY; PRT; 1070 AA.
 AC QAN1B8;
 DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
 DT 02-AUG-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Hypothetical protein.
 GN ORFNames=TP04_0796;
 OS Theileria parva.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 CC Theileria.
 OX NCBI_TaxID=5875;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=Muguga;
 RC PubMed=15994558; DOI=10.1126/science.1110439;
 RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
 RA Hall N., Ren Q., Paulsen I.T., Pain A., Villiers M., Wilson R.J.,
 RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
 RA Jiang L., Lynn J., Weaver B., Shoabli A., Domingo A.R., Masawa D.,
 RA Crabtree J., Wortman J.R., Haas B., Anguilo S.V., Creasy T.H., Lu C.,
 RA Suh B., Silva J.C., Uterback T.R., Feldblyum T.V., Perera M.,
 RA Allen J., Nierman W.C., Taracha E.L., Salzberg S.L., White O.R.,
 RA Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;
 RA "Genome Sequence of Theileria parva, a Bovine Pathogen That Transforms
 RT Lymphocytes.";
 RL Science 309:134-137 (2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=Muguga;
 RC Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
 RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
 RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,

RA Lynn J., Weaver B., Shoabli A., Masawa D., Crabtree J., Wortman J.R.,
 RA Haas B., Anguilo S., Creasy T.H., Lu C., Suh B., Silva J.C.,
 RA Uterback T., Feldblyum T., Perera M., Allen J., Taracha E.L.,
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
 RA Fraser C.M., Nene V.;
 RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
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 DR EMBL; AAGK01000004; EAN32150.1; -; Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005044; F:scavenger receptor activity; IEA.
 DR InterPro; IPR004043; LCCL.
 DR InterPro; IPR001024; Lipase_LH2.
 DR InterPro; IPR001190; Srcr_rcpt.
 DR Pfam; PF03815; LCCL; 4.
 DR Pfam; PF01477; PLAT; 1.
 DR Pfam; PF00530; SRCR; 2.
 DR PRINTS; PR00258; SPBRACRCPTR.
 DR SMART; SW00202; SR; 2.
 DR PROSITE; PSS0820; LCCL; 4.
 DR PROSITE; PSS0095; PLAT; 1.
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 KW Hypothetical protein.
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 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 626 HSGVLNNSG 635

RESULT 15
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 AC Q4UBP9;
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2005, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Hypothetical protein.
 GN ORFNames=TA09935;
 OS Theileria annulata.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 CC Theileria.
 OX NCBI_TaxID=5874;
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 RA STRAIN=Ankara isolate clone C9;
 RC PubMed=15994597; DOI=10.1258/jrem.98.7.320;
 RA Pain A., Renaud H., Berriman M., Murphy L., Yeats C.A., Weir W.,
 RA Karhounou A., Aletti M., Bishop R., Bouchier C., Cochet M.,
 RA Coulson R.M.R., Cronin A., de Villiers E.P., Fraser A., Foster N.,
 RA Gardner M., Goble A., Griffiths-Jones S., Harris D.E., Ketzner F.,
 RA Larke N., Lord A., Maier P., McKellar S., Mooney P., Morton F.,
 RA Nene V., O'Neill S., Price C., Quail M.A., Rabinowitz E.,
 RA Rawlings N.D., Rutter S., Saunders D., Seeger K., Shah T., Squares R.,
 RA Squares S., Tivey A., Walker A.R., Woodward J., Dobbelaere D.A.E.,
 RA Langsley G., Rajandream M-A., McKeever D., Shiels B., Tait A.,
 RA Barrett B., Hall N.;
 RA "Genome of the host-cell transforming parasite Theileria annulata
 RT compared with T. parva.";
 RL Science 309:131-133 (2005).
 RN [2]
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DR EMBL; CR940353; CA176804.1; -: Genomic_DNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005044; F:scavenger receptor activity; IEA.
 DR InterPro; IPR013320; ConA_like_subgrp.
 DR InterPro; IPR004043; LCCL.
 DR InterPro; IPR008976; Lipase_lipase.
 DR InterPro; IPR01024; Lipase_LH2.
 DR InterPro; IPR01190; Srcr_rcpt.
 DR Pfam; PF03815; LCCL; 4.
 DR Pfam; PF01477; PLAT; 1.
 DR PRINTS; PR00258; SPBRACTRCPTR.
 DR SMART; SM00202; SR; 1.
 DR PROSITE; PSS0820; LCCL; 4.
 DR PROSITE; PSS0095; PLAT; 1.
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 KW Hypothetical protein.
 SQ SEQUENCE 1197 AA; 132106 MW; E613399C9F4B1856 CRC64;

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 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 705 HSGVLDNSGG 714

Search completed: June 7, 2006, 01:43:44
 Job time : 307 secs

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OM protein - protein search, using sw model

Run on: June 7, 2006, 01:43:58 ; Search time 51 Seconds
(without alignments)
1163.642 Million cell updates/sec

Title: US-10-063-540-34

Perfect score: 678
Sequence: 1 MRTVLTMKASVEMFLVL.....QVPRITICTEFNSQPRN 678

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2836

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: Issued_Patents_AA.*
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3: /EMC_Celerra_SIDS3/ptodata/2/1aa/6.COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/1aa/7.COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/1aa/H.COMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/1aa/RE.COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 3 | 678 | 100.0 | 678 | 2 | US-09-997-333-179 Sequence 179, App |
| 4 | 678 | 100.0 | 678 | 2 | US-09-992-598-179 Sequence 179, App |
| 5 | 678 | 100.0 | 678 | 2 | US-09-988-735-179 Sequence 179, App |
| 6 | 678 | 100.0 | 678 | 3 | US-09-989-726-179 Sequence 179, App |
| 7 | 678 | 100.0 | 678 | 3 | US-09-997-514-179 Sequence 179, App |
| 8 | 678 | 100.0 | 678 | 3 | US-09-989-728-179 Sequence 179, App |
| 9 | 678 | 100.0 | 678 | 3 | US-09-997-349-179 Sequence 179, App |
| 10 | 678 | 100.0 | 678 | 3 | US-09-989-653-179 Sequence 179, App |
| 11 | 678 | 100.0 | 678 | 3 | US-09-989-233A-179 Sequence 5, Appl1 |
| 12 | 678 | 100.0 | 678 | 3 | US-09-994-264-5 Sequence 5, Appl1 |
| 13 | 678 | 100.0 | 678 | 3 | US-09-907-794A-227 Sequence 227, App |
| 14 | 678 | 100.0 | 678 | 3 | US-09-905-125A-227 Sequence 227, App |
| 15 | 678 | 100.0 | 678 | 3 | US-09-902-775A-227 Sequence 227, App |
| 16 | 678 | 100.0 | 678 | 3 | US-09-906-700-227 Sequence 227, App |
| 17 | 678 | 100.0 | 678 | 3 | US-09-579-288-2 Sequence 2, Appl1 |
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| 19 | 678 | 100.0 | 678 | 3 | US-09-903-603A-227 Sequence 227, App |
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| 22 | 678 | 100.0 | 678 | 3 | US-09-909-064-227 Sequence 227, App |
| 23 | 678 | 100.0 | 678 | 3 | US-09-905-381A-227 Sequence 227, App |
| 24 | 678 | 100.0 | 678 | 3 | US-09-906-618-227 Sequence 227, App |
| 25 | 678 | 100.0 | 678 | 3 | US-09-906-646-227 Sequence 227, App |
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| 30 | 8 | 1.2 | 550 | 2 | US-09-903-562B-227 Sequence 227, App |
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| 32 | 8 | 1.2 | 550 | 3 | US-09-394-264-2 Sequence 227, App |
| 33 | 8 | 1.2 | 550 | 3 | US-09-907-841-227 Sequence 227, App |
| 34 | 8 | 1.2 | 552 | 3 | US-09-394-264-7 Sequence 7, Appl1 |
| 35 | 8 | 1.2 | 568 | 2 | US-09-949-016-8845 Sequence 8845, App |
| 36 | 8 | 1.2 | 575 | 2 | US-09-949-016-8294 Sequence 8294, App |
| 37 | 8 | 1.2 | 733 | 2 | US-09-270-767-41626 Sequence 41626, App |
| 38 | 7 | 1.0 | 27 | 3 | US-09-463-058-178 Sequence 178, App |
| 39 | 7 | 1.0 | 62 | 2 | US-09-621-976-6538 Sequence 6538, App |
| 40 | 7 | 1.0 | 27 | 2 | US-09-248-796A-23281 Sequence 23281, App |
| 41 | 7 | 1.0 | 66 | 2 | US-09-513-999C-7765 Sequence 7765, App |
| 42 | 7 | 1.0 | 71 | 2 | US-09-248-796A-23031 Sequence 23031, App |
| 43 | 7 | 1.0 | 73 | 2 | US-09-489-039A-13279 Sequence 13279, App |
| 44 | 7 | 1.0 | 92 | 2 | US-09-270-767-59560 Sequence 59560, App |
| 45 | 7 | 1.0 | 99 | 2 | US-09-270-767-60317 Sequence 60317, App |

ALIGNMENTS

RESULT 1
US-09-991-181-179
Sequence 179, Application US/09991181
Patent No. 6913919
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Deonoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322

[illegible]

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTLMKASVIEMLVLLVTGHSNKETAKKIKRPFVPOJNCVAKGIIDPEFIV 60
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DB 61 KCPAGCDDPKHYVGTGVVYASYSVCGAAVHSGVLDSGGKILVRKVAQSGYKGSYNG 120
QY 121 VQSLSPRMRSEFVLESKPKGVTPSALTYSSTKSPAAQAGETTKAYORPPIGTAAQ 180
DB 121 VQSLSPRMRSEFVLESKPKGVTPSALTYSSTKSPAAQAGETTKAYORPPIGTAAQ 180
QY 181 PVTLMQLAATVAVATPTTLPRPSPASATTSIPRPOSVGHRSGEMDLMTATYTSSQNR 240
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QY 241 PRADPGIQRDPSGAARQKVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDISFLIDG 300
DB 241 PRADPGIQRDPSGAARQKVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDISFLIDG 300
QY 301 STSIGKRFRIOQLADVAQALDIGPAGPLMGVVOGDNPAHTFNLKTHNSRDLTAI 360
DB 301 STSIGKRFRIOQLADVAQALDIGPAGPLMGVVOGDNPAHTFNLKTHNSRDLTAI 360
QY 361 EKITRQGLSNVGRALSFTVKNFPSKANGRSKAPNVVVVVVMDPMDTKYEASRLARES 420
DB 361 EKITRQGLSNVGRALSFTVKNFPSKANGRSKAPNVVVVVVMDPMDTKYEASRLARES 420
QY 421 GINIPTTIGAAENKQYVVEPNFANKAVCRITNGPSLHVQSWFGHLTKLOPLVKEVCD 480
DB 421 GINIPTTIGAAENKQYVVEPNFANKAVCRITNGPSLHVQSWFGHLTKLOPLVKEVCD 480
QY 481 TDRLASCKTLNADIGFVIDGSSVGTGNFRVLOVNTLTKFEESDPTDTRIGAQOYT 540
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DB 541 YEQRLFFGPDKYSSKPDILNAIKRVGWSGTSIGAALNFALBQLFKSKRPNKRKMLILI 600
QY 601 TDRGSTVDVRIIPMAAHLKCVITVYIGVAAAOEELEVIATHPARDHSFVDEFDNIHQY 660
DB 601 TDRGSTVDVRIIPMAAHLKCVITVYIGVAAAOEELEVIATHPARDHSFVDEFDNIHQY 660
QY 661 VPRIIIONICTEFNOSPRN 678
DB 661 VPRIIIONICTEFNOSPRN 678

RESULT 2
US-09-990-444-179
Sequence 179, Application US/09990444
Patent No. 6930170

;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman

;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C19
;; CURRENT APPLICATION NUMBER: US/09/990,444
;; CURRENT FILING DATE: 2001-11-14
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 2; Length 678;
Best Local Similarity 100.0%; Pred No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVVLTMKASVIEMLVLLVTVGHSNKEETAKKIKRPFVTPQINDVYAKIIDEFFIV 60
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Db
QY 61 KCPAGCDDPKYHYGYGDDVYASYSVCGAAVHSGVLDNSGKILVRVVAQSGYKGSYSNG 120
61 KCPAGCDDPKYHYGYGDDVYASYSVCGAAVHSGVLDNSGKILVRVVAQSGYKGSYSNG 120
Db
QY 121 VQSLSPRMRESFIVESKPKKGVTPSALTYSKSPAAQGETTKAYORPPIPGTTAQ 180
121 VQSLSPRMRESFIVESKPKKGVTPSALTYSKSPAAQGETTKAYORPPIPGTTAQ 180
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QY 121 VQSLSPRMRESFIVESKPKKGVTPSALTYSKSPAAQGETTKAYORPPIPGTTAQ 180
121 VQSLSPRMRESFIVESKPKKGVTPSALTYSKSPAAQGETTKAYORPPIPGTTAQ 180
Db
QY 181 PVTIMOLLAVTAVATPTTLPRPSPAASTTSIPRQSVGHSQEMDLWSTATYTSQNR 240
181 PVTIMOLLAVTAVATPTTLPRPSPAASTTSIPRQSVGHSQEMDLWSTATYTSQNR 240
Db
QY 241 PRADPGIQRQDPBGGAFOKRVGADVSLGVPKBELSTQSLPEVSLGDDPNCKIDLSFLIDG 300
241 PRADPGIQRQDPBGGAFOKRVGADVSLGVPKBELSTQSLPEVSLGDDPNCKIDLSFLIDG 300
Db
QY 301 STSIGKRRRIQQLADVAQALDIPGAPLGMGVQGNPATFNLKTHTNSRDLKTAI 360
301 STSIGKRRRIQQLADVAQALDIPGAPLGMGVQGNPATFNLKTHTNSRDLKTAI 360
Db

Fri Jun 9 11:08:02 2006

QY 361 EKITORGGLSNVGRALISFVTJNFKFSKANGNSGAPNVVVWVWGNPTDKVEASRLAES 420
D 361 EKITORGGLSNVGRALISFVTJNFKFSKANGNSGAPNVVVWVWGNPTDKVEASRLAES 420
QY 421 GINIFFTIEGAENKQYVVEPNFANKAVCTTNGFSLHQSWSGLKHTLOPLVKRYCD 480
D 421 GINIFFTIEGAENKQYVVEPNFANKAVCTTNGFSLHQSWSGLKHTLOPLVKRYCD 480
QY 481 TDRJACSKTCLNSADIGFVIDGSSSVGTGNFRVTYQFNTNLTKEFEISDTPRIGAVOYT 540
D 481 TDRJACSKTCLNSADIGFVIDGSSSVGTGNFRVTYQFNTNLTKEFEISDTPRIGAVOYT 540
QY 541 YEORLEFQFDKYSKPDILNAIKRVYWSGGTGTGAINFALBQLFKSKPKKRLMLI 600
D 541 YEORLEFQFDKYSKPDILNAIKRVYWSGGTGTGAINFALBQLFKSKPKKRLMLI 600
QY 601 TDGSSYDDVRIPAMAHLKGVITTAIGVMAAOELEVIAIHPADHSFPVDEPNLHOY 660
D 601 TDGSSYDDVRIPAMAHLKGVITTAIGVMAAOELEVIAIHPADHSFPVDEPNLHOY 660
QY 661 VPRIONCTEFSNOPS 678
D 661 VPRIONCTEFSNOPS 678

RESULT 3
US-09-997-333-179
Sequence 179, Application US/09997333
Patent No. 6953836
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Bacon, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlesen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C27
CURRENT APPLICATION NUMBER: US/09/997,333
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1998-03-20

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Query Match 100.0%; Score 678; DB 2; Length 678;
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 DB 181 PVTLMQLAVTVAVATPTTLPRPSPSAASTTSIPRPOSVGHRSQEMDLWSTATYTSQNR 240
 QY 241 PRADPGIQRODPBGGAAPQKVGADVSLGLVPKELSTQSLPEVSLDPPNCKIDLSFLIDG 300
 DB 241 PRADPGIQRODPBGGAAPQKVGADVSLGLVPKELSTQSLPEVSLDPPNCKIDLSFLIDG 300
 QY 301 STSIGKRRFRIOQLADVAQALDIGPAGPLMGVVOYGDNPATHFNLKHTNSRDLKTAI 360
 DB 301 STSIGKRRFRIOQLADVAQALDIGPAGPLMGVVOYGDNPATHFNLKHTNSRDLKTAI 360
 QY 361 EKITRGGLSNVGRASISFVTXNFFSKANGRSAPNVVVVVMDGPTDKYEA SRLARES 420
 DB 361 EKITRGGLSNVGRASISFVTXNFFSKANGRSAPNVVVVVMDGPTDKYEA SRLARES 420
 QY 421 GINIFFTTIGGAENENQYVVEPNPANKAVCRNNGFSLHVSQSPFGJHKLQPLVYKVCV 480
 DB 421 GINIFFTTIGGAENENQYVVEPNPANKAVCRNNGFSLHVSQSPFGJHKLQPLVYKVCV 480
 QY 481 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLOFTVNLTKEFISDTRTIGAVOYT 540
 DB 481 TDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLOFTVNLTKEFISDTRTIGAVOYT 540
 QY 541 YEORLEFGFDKYSKPDILNAIRVGVWSGSTGAALNFALQLEFKSKPNRKMLILI 600
 DB 541 YEORLEFGFDKYSKPDILNAIRVGVWSGSTGAALNFALQLEFKSKPNRKMLILI 600
 QY 601 TDRGSYDVARIPMAAHLKGVITTYAIGVMAAEELEVIATHPARHSPFVDFEDNLHOY 660
 DB 601 TDRGSYDVARIPMAAHLKGVITTYAIGVMAAEELEVIATHPARHSPFVDFEDNLHOY 660
 QY 661 VPRIIQNICTEFNSOPRN 678
 DB 661 VPRIIQNICTEFNSOPRN 678

RESULT 4
 US-09-992-598-179
 Sequence 179, Application US/09992598
 Patent No. 6956108
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C20
CURRENT FILING DATE: US/09/1992, 598
PRIOR APPLICATION NUMBER: 2001-11-14
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/083322
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 2; Length 678;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 678; Conservative 0;

QY 1 MRTVVLTKASVLEPLVLVTGHSNKEAKIKRPFVPOINCDVKAGKIIDPEFIY 60
DB 1 MRTVVLTKASVLEPLVLVTGHSNKEAKIKRPFVPOINCDVKAGKIIDPEFIY 60
QY 61 KCPAGCDDPKHYVGTIVYASYSVCGAAVHSGVLNDSGGKILYRKVAGSGYGSYSNG 120
DB 61 KCPAGCDDPKHYVGTIVYASYSVCGAAVHSGVLNDSGGKILYRKVAGSGYGSYSNG 120
QY 121 VQSLSLPRMSEFVLESKRKGVTPSALTYSSSKSPAAOAGRTTAYORPPITGTTAQ 180
DB 121 VQSLSLPRMSEFVLESKRKGVTPSALTYSSSKSPAAOAGRTTAYORPPITGTTAQ 180
QY 181 PVTLMQLATVAVATPTTLPRPSPASATTSIPRPOVGHRSQEMDLMTATYTSSQNR 240
DB 181 PVTLMQLATVAVATPTTLPRPSPASATTSIPRPOVGHRSQEMDLMTATYTSSQNR 240
QY 241 PRADPGIQRDPGSAFQKVGADVSLGLYPKEELSTQSLSEPVSLGDPNCKIDISFLIDG 300
DB 241 PRADPGIQRDPGSAFQKVGADVSLGLYPKEELSTQSLSEPVSLGDPNCKIDISFLIDG 300
QY 301 STSIGKRFPFIQKQLADVQAQDIDGPAGPLMGVVQGVNDPATHTFNLTHTNSKDLTAT 360
DB 301 STSIGKRFPFIQKQLADVQAQDIDGPAGPLMGVVQGVNDPATHTFNLTHTNSKDLTAT 360

QY 361 EKITQRGGLSNVGRALISFVTKNFFSSKANGRSGAPNVVVVMDGMPDTDKVEASRLARES 420
DB 361 EKITQRGGLSNVGRALISFVTKNFFSSKANGRSGAPNVVVVMDGMPDTDKVEASRLARES 420
QY 421 GINFFITIEGAANEQYVVEPNFANKAVCRNNGFVSLHVQSMFGLHKTLOPLVXVCD 480
DB 421 GINFFITIEGAANEQYVVEPNFANKAVCRNNGFVSLHVQSMFGLHKTLOPLVXVCD 480
QY 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVTLQFTNLTKFEISDPTDTIGAVQYT 540
DB 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVTLQFTNLTKFEISDPTDTIGAVQYT 540
QY 541 YEORLEFGDKYSSKPDILNAIKRVGYSGTSTGAALNFBQLFKKSKPNRKLMLI 600
DB 541 YEORLEFGDKYSSKPDILNAIKRVGYSGTSTGAALNFBQLFKKSKPNRKLMLI 600
QY 601 TDGRSYDDVRIIPMAAHLKGVITTYAIGVAAQEELEVITHPARDHSFFVDEFDNLHOY 660
DB 601 TDGRSYDDVRIIPMAAHLKGVITTYAIGVAAQEELEVITHPARDHSFFVDEFDNLHOY 660
QY 661 VPRIONICTEFNSOPRN 678
DB 661 VPRIONICTEFNSOPRN 678

RESULT 5

US-09-989-735-179

Sequence 179, Application US/09989735

Patent No. 6972185

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Bostein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: 82730P1C61

CURRENT APPLICATION NUMBER: US/09/989,735

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

[illegible]

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRYVLMKASVEMFLVLTGVSHNKETAKTKRPFYVPOINCDVAKGIIDPEFV 60
DB 1 MRYVLMKASVEMFLVLTGVSHNKETAKTKRPFYVPOINCDVAKGIIDPEFV 60
QY 61 KCPAGCDDPKHYVGTVDVYASVSSVCGAAVHSGVLDSGKILVRKVAQSGYKGSYNG 120
DB 61 KCPAGCDDPKHYVGTVDVYASVSSVCGAAVHSGVLDSGKILVRKVAQSGYKGSYNG 120
QY 121 VQSLSLPRMBESFVLESKPKKGYTPSALTYSKSPAAQAGETTYAYQPPITTAQ 180
DB 121 VQSLSLPRMBESFVLESKPKKGYTPSALTYSKSPAAQAGETTYAYQPPITTAQ 180
QY 181 PVTLMQLAATVAAVPTTLPRPSPASASTTSIRPQSVGHRSGEMDLMSTATYSSONR 240
DB 181 PVTLMQLAATVAAVPTTLPRPSPASASTTSIRPQSVGHRSGEMDLMSTATYSSONR 240
QY 241 PRADPGIQRODPSGAFOKPVGADVSLGLVPKEELSTQSLRPVSLGDPNCKIDSLFIDG 300
DB 241 PRADPGIQRODPSGAFOKPVGADVSLGLVPKEELSTQSLRPVSLGDPNCKIDSLFIDG 300
QY 301 STSIGKRFRFIOKQLADVAQALDIGRAGPLMGVVOYQDNPATFENLKTHTNSHDLKTAI 360
DB 301 STSIGKRFRFIOKQLADVAQALDIGRAGPLMGVVOYQDNPATFENLKTHTNSHDLKTAI 360
QY 361 EKITRQGLSNVGRASFVTKNFSPSKANGNSGAPNVVVVVVDMPDKVEASRLARES 420
DB 361 EKITRQGLSNVGRASFVTKNFSPSKANGNSGAPNVVVVVVDMPDKVEASRLARES 420
QY 421 GINIFITIEGAANEKQYVVEPNPANKAVCRITNGFYSLHVSQWFGHLKTLQPLVKVCD 480
DB 421 GINIFITIEGAANEKQYVVEPNPANKAVCRITNGFYSLHVSQWFGHLKTLQPLVKVCD 480
QY 481 TDRLAGCKTCLNSADIGFVIDGSSVGTGNFRYVLOFVTNLTKEFEISDPTFRIGAVOYT 540
DB 481 TDRLAGCKTCLNSADIGFVIDGSSVGTGNFRYVLOFVTNLTKEFEISDPTFRIGAVOYT 540
QY 541 YEQRLLEGFPKYSKPIILNAIKRVGWSGCTSGAALNFBELFKSKRNKMKMLILI 600
DB 541 YEQRLLEGFPKYSKPIILNAIKRVGWSGCTSGAALNFBELFKSKRNKMKMLILI 600
QY 601 TDRGRSYDVARI PAMAAHLKGVITTAIGVAAAQEELEVIATHPARDHSFVDEFDNLHOY 660
DB 601 TDRGRSYDVARI PAMAAHLKGVITTAIGVAAAQEELEVIATHPARDHSFVDEFDNLHOY 660
QY 661 VPRIIIONICTEFNSOPRN 678
DB 661 VPRIIIONICTEFNSOPRN 678

RESULT 6
US-09-989-726-179
Sequence 179, Application US/09989726
Patent No. 701811

;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Denoyers, Luc
;; APPLICANT: Eaton, Dan L.

;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary B.
;; APPLICANT: Goddard, Audrey
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;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C60
;; CURRENT APPLICATION NUMBER: US/09/989,726
;; PRIOR FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRYVVLTMKASVIEMLFVLVTGHSNKEKTAKKIKRKFVTPQINCVCVKGKIIDPERIV 60
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Qy 61 KCPAGCDDPKYHYGVTVVAVSYSSVCGAAVHSGVLVNSGGKILVRKAYAGOSGYGSYNG 120
Db 61 KCPAGCDDPKYHYGVTVVAVSYSSVCGAAVHSGVLVNSGGKILVRKAYAGOSGYGSYNG 120
Qy 121 VQSLSLPRMRRESFVLESKPKKGVTPSALTYSSSKSPAAOAGETTYAYORPPIGTAAQ 180
Db 121 VQSLSLPRMRRESFVLESKPKKGVTPSALTYSSSKSPAAOAGETTYAYORPPIGTAAQ 180
Qy 181 PYTLMQLLAVTVAAVATPTLPRPSPASSTSTIPRPSVGHRSQEMLMSTATYTSSONR 240
Db 181 PYTLMQLLAVTVAAVATPTLPRPSPASSTSTIPRPSVGHRSQEMLMSTATYTSSONR 240
Qy 241 PRADPGIORODPSGAARQKPVGADVSLGLVPKEELSTQSLSPVSLGDPNCKIDLSFLIDG 300
Db 241 PRADPGIORODPSGAARQKPVGADVSLGLVPKEELSTQSLSPVSLGDPNCKIDLSFLIDG 300
Qy 301 STSIGKRFRIRIQQLADVAAQALDIGPAGPLMGVGVYGDNPATHTNKHNSDLXTAI 360
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Db 301 STSIGRRFRIOQLADVAQALDIGPAGLGMVVOXDNDPETHFNKTHNSDLTKAT 360
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Db 361 EKITORGGLSNVGRRAISFTVKNFPSKANGRSAGAPNVVVVVVDGMPDTKYEASRLARES 420
Qy 421 GINIFITIEGAANEKQYVVEPNFANKAVCRITNGFYSLSHVQSWFGLKTLQPLVKRVC 480
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Qy 481 TDLRACSKTLLNSADIGFVIDGSSVGTGNFRTVLQVTVNLTKFEISDPTDRIGAVOYT 540
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Qy 541 YEORLEGFPGKYSKSPILNAIKRVGWSGSGTGAALNFBOLFKSKPKNKKMLILI 600
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Qy 601 TDRGSYDDVRI PMAAHLKGVITYAIGVANAQOELEVIATHPARDHSFVDEFDNLHOY 660
Db 601 TDRGSYDDVRI PMAAHLKGVITYAIGVANAQOELEVIATHPARDHSFVDEFDNLHOY 660
Qy 661 VPRIIQNICTEFNSQPRN 678
Db 661 VPRIIQNICTEFNSQPRN 678

RESULT 7

US-09-997-514-179
Sequence 179, Application US/09997514
Patent No. 7019116
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Godowski, Paul J.
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C46
CURRENT APPLICATION NUMBER: US/09/997,514
CURRENT FILING DATE: 2001-11-15
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Query Match 100.0%; Score 678; DB 3; Length 678;
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Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MRTVLTMKASVEMFLVLTGVSNETAKIKRPFVYPOINCDVKAIGKIIDPEFIV 60
Db 1 MRTVLTMKASVEMFLVLTGVSNETAKIKRPFVYPOINCDVKAIGKIIDPEFIV 60
QY KCPAGCDDPKYHVYGTVDVASYSSVCGAAVHSGVLDNSGGKILVRKVAQSGYKGSYNG 120
61 KCPAGCDDPKYHVYGTVDVASYSSVCGAAVHSGVLDNSGGKILVRKVAQSGYKGSYNG 120
Db 61 KCPAGCDDPKYHVYGTVDVASYSSVCGAAVHSGVLDNSGGKILVRKVAQSGYKGSYNG 120
QY 121 VQSLSPRMBSPVLESKEPKGYTYSALTYSKSPAAQAGETTAQYQRPPIPTTAQ 180
121 VQSLSPRMBSPVLESKEPKGYTYSALTYSKSPAAQAGETTAQYQRPPIPTTAQ 180
Db 121 VQSLSPRMBSPVLESKEPKGYTYSALTYSKSPAAQAGETTAQYQRPPIPTTAQ 180
QY 181 PVTLMOLAVTVAAATPTTLPRPSPASSTTSIRPOSVGRSQEMLMSTATYSSONR 240
181 PVTLMOLAVTVAAATPTTLPRPSPASSTTSIRPOSVGRSQEMLMSTATYSSONR 240
Db 181 PVTLMOLAVTVAAATPTTLPRPSPASSTTSIRPOSVGRSQEMLMSTATYSSONR 240
QY 241 PRADPGIORODPSGAFOKPVGADVSLGLVPKEELSTQSLPVSAGDPNCKIDSLFLDG 300
241 PRADPGIORODPSGAFOKPVGADVSLGLVPKEELSTQSLPVSAGDPNCKIDSLFLDG 300
Db 241 PRADPGIORODPSGAFOKPVGADVSLGLVPKEELSTQSLPVSAGDPNCKIDSLFLDG 300
QY 301 STSICKRRPRIQKLLADVQAOLDIGPAGPLMGVVOYGDNPATFNNLKTHTNSDKLTAI 360
301 STSICKRRPRIQKLLADVQAOLDIGPAGPLMGVVOYGDNPATFNNLKTHTNSDKLTAI 360
Db 301 STSICKRRPRIQKLLADVQAOLDIGPAGPLMGVVOYGDNPATFNNLKTHTNSDKLTAI 360
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Db 361 EKITORGSLNVGSAISFTVKNFSPSKANGNRSGAPNVVWVDMPTDKVEASRLARES 420
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Db 421 GINIFFTTIGAAENEQYVVEPNFANKAVCRTNGFYSLHVSQWFGJHKTLOPLVKRCD 480
QY 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRFVLQEVNTLTKFEISDTRIGAVOYT 540
481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRFVLQEVNTLTKFEISDTRIGAVOYT 540
Db 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRFVLQEVNTLTKFEISDTRIGAVOYT 540
QY 541 YEOGLEFGDPKYSKXPILINAIRVGVWSGSTGGAINFALBOLFKKSKPKKXKMLMI 600
541 YEOGLEFGDPKYSKXPILINAIRVGVWSGSTGGAINFALBOLFKKSKPKKXKMLMI 600
Db 541 YEOGLEFGDPKYSKXPILINAIRVGVWSGSTGGAINFALBOLFKKSKPKKXKMLMI 600
QY 601 TDGRSYDDVRIPAAAHKGVITYTAIGVMAAQELEVIAITHPARDSFFVDEFDNLHQY 660
601 TDGRSYDDVRIPAAAHKGVITYTAIGVMAAQELEVIAITHPARDSFFVDEFDNLHQY 660
Db 601 TDGRSYDDVRIPAAAHKGVITYTAIGVMAAQELEVIAITHPARDSFFVDEFDNLHQY 660
QY 661 VPRILIONICTEENSOPRN 678
661 VPRILIONICTEENSOPRN 678
Db 661 VPRILIONICTEENSOPRN 678

RESULT 8
US-09-989-728-179
Sequence 179, Application US/09989728
Patent No. 7029873
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC72
CURRENT APPLICATION NUMBER: US/09/989,728
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 678; DB 3; Length 678;
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 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRTVLTLMKASVIEMLVLLVTGVHSNKEITAKKIKRPFVTPQINCVDYKAGKIIDPEFIY 60
DB 1 MRTVLTLMKASVIEMLVLLVTGVHSNKEITAKKIKRPFVTPQINCVDYKAGKIIDPEFIY 60
QY 61 KCPAGCDDPKYHYGTDVYASYSVCGAAVHSGVLNDSGGKIIYRKXAGOSGYGSYNSG 120
DB 61 KCPAGCDDPKYHYGTDVYASYSVCGAAVHSGVLNDSGGKIIYRKXAGOSGYGSYNSG 120
QY 121 VQSLSLPRWRESFVLESKEPKKGVTPSALTYSKSPAAOAGETTRAYORPPIPTTAQ 180
DB 121 VQSLSLPRWRESFVLESKEPKKGVTPSALTYSKSPAAOAGETTRAYORPPIPTTAQ 180
QY 181 PVTLMQLLAVTVAAVATPTTLPREPSPASATTSIPRPOSVGHRSQEMDLWSTATTSSQNR 240
DB 181 PVTLMQLLAVTVAAVATPTTLPREPSPASATTSIPRPOSVGHRSQEMDLWSTATTSSQNR 240
QY 241 PRADPGQRDDPSGAAROKPVGAVSLGLVPEKESLQSLSEPVSLGDPNCKIDSLFIIDG 300
DB 241 PRADPGQRDDPSGAAROKPVGAVSLGLVPEKESLQSLSEPVSLGDPNCKIDSLFIIDG 300
QY 301 STSIGKRFRIOQLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHNSRDLXTAI 360

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DB 301 STSIGKRFRIOQLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHNSRDLXTAI 360
QY 361 EKITQRGGLSNVGAISFVTKNPFSSKANGNSGAPNVVVVWDMPDKYKEASRLARES 420
DB 361 EKITQRGGLSNVGAISFVTKNPFSSKANGNSGAPNVVVVWDMPDKYKEASRLARES 420
QY 421 GINIFFTTIEGAANEQYVVEPFAKAVCRTGPFYSLHVSQFGLHKTLOPLVKEVCD 480
DB 421 GINIFFTTIEGAANEQYVVEPFAKAVCRTGPFYSLHVSQFGLHKTLOPLVKEVCD 480
QY 481 TDLRACSKTCLNSADIGFVIDSSSVGTGNFRVLOFTNLTKFEESIDTDRIGAVOYT 540
DB 481 TDLRACSKTCLNSADIGFVIDSSSVGTGNFRVLOFTNLTKFEESIDTDRIGAVOYT 540
QY 541 YEORLFEGPDKYSKPIIINAIRKRVGWSGCTSGAINALSOLFKKSKPNKRXKMLI 600
DB 541 YEORLFEGPDKYSKPIIINAIRKRVGWSGCTSGAINALSOLFKKSKPNKRXKMLI 600
QY 601 TDGRSYDVRIPMAAHLKGVITYAIGVAAQEELEVIATHPARDHSFVDEFDNLHOY 660
DB 601 TDGRSYDVRIPMAAHLKGVITYAIGVAAQEELEVIATHPARDHSFVDEFDNLHOY 660
QY 661 VPRIIQNICTEFNSQPRN 678
DB 661 VPRIIQNICTEFNSQPRN 678

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RESULT 9
 US-09-997-349-179
 ; Sequence 179, Application US/09997349
 ; Patent No. 7034106
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerltsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Guney, Austin L.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Matanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC37
 ; CURRENT APPLICATION NUMBER: US/09/997,349
 ; PRIOR FILING DATE: 2001-11-15
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945

[illegible]


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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 678; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      121 VQSLPRMRESFTVLESKPKKGYTPSALTYSSSKSPAQAQETTKAYQRPPIGTTAQ 180
DB      121 VQSLPRMRESFTVLESKPKKGYTPSALTYSSSKSPAQAQETTKAYQRPPIGTTAQ 180

QY      181 PVTIMOLLAVTVAATPTTLPRSPSAASTTSIPRPOSVGHRSQMDIMSTATTSSQNR 240
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QY      241 PRADPGIORODPSGAFOKPYGADVSLGLVPEKEELSTQSLSPVLDGPNCKIDISPLIDG 300
DB      241 PRADPGIORODPSGAFOKPYGADVSLGLVPEKEELSTQSLSPVLDGPNCKIDISPLIDG 300

QY      301 STSICKRRFRIQOKLADVAQALDIGPAGPLMGVVOYGDNPATHTFNLKTHNSRDLKTAI 360
DB      301 STSICKRRFRIQOKLADVAQALDIGPAGPLMGVVOYGDNPATHTFNLKTHNSRDLKTAI 360

QY      361 EKITQRGGLSNVGAISFTVTKNFPFSKANGNSGAPNVVVVVWDGMPDCKVEASRLARES 420
DB      361 EKITQRGGLSNVGAISFTVTKNFPFSKANGNSGAPNVVVVVWDGMPDCKVEASRLARES 420

QY      421 GINIFFTTIEGAENEMQYVVEPNPANKAVCRTEGFVSLHQSMPGLKTLQPLVKRYCD 480
DB      421 GINIFFTTIEGAENEMQYVVEPNPANKAVCRTEGFVSLHQSMPGLKTLQPLVKRYCD 480

QY      481 TDRACSKTCINSAADIGFVIDGSSSVGTGNFRVLQFVTNLTKFEFISDTRIGAVOYT 540
DB      481 TDRACSKTCINSAADIGFVIDGSSSVGTGNFRVLQFVTNLTKFEFISDTRIGAVOYT 540

QY      541 YEORLEFGPDKYSKPDILNAIKRVGYSWGGTSTGAALNPALEOLFKXSKPKKKMLILI 600
DB      541 YEORLEFGPDKYSKPDILNAIKRVGYSWGGTSTGAALNPALEOLFKXSKPKKKMLILI 600

QY      601 TDGSSYDVRIPAAAHKGVITTAIGVAMAQOELEVIATHPARDSFFVDEEDNLHOY 660
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QY      661 VPRIIQICTEFNSQPRN 678
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; Patent No. 7034122
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997,653
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787

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PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 3; Length 678;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVVLTKRASVTEMFLVLLVTCVSHNSKETAKKIKPKKTTVPQINDVAKGIIDEEFV 60
DB 1 MRTVVLTKRASVTEMFLVLLVTCVSHNSKETAKKIKPKKTTVPQINDVAKGIIDEEFV 60
QY 1 KCPAGCOPDKYHYGTDVYASYSVCGAAMHSGVLNDSGAKILVRKAGOSGYKSYSNG 120
DB 1 KCPAGCOPDKYHYGTDVYASYSVCGAAMHSGVLNDSGAKILVRKAGOSGYKSYSNG 120
QY 121 VQSLSPRMRESFVLESKRKGVTPSALTYSSSKSPAAGETTKAYORPPIPETTAQ 180
DB 121 VQSLSPRMRESFVLESKRKGVTPSALTYSSSKSPAAGETTKAYORPPIPETTAQ 180
QY 181 PVTLMOLLAVTVAVAPPTLPRSPSAASTTSPRQSVGHSQEMDLSTATYSSQNR 240
DB 181 PVTLMOLLAVTVAVAPPTLPRSPSAASTTSPRQSVGHSQEMDLSTATYSSQNR 240
QY 241 PRADPGIORODPSGAFFQVPGADVSLGLVPKEELSTOSLEPVSLGDPNCKIDLSEFLIDG 300
DB 241 PRADPGIORODPSGAFFQVPGADVSLGLVPKEELSTOSLEPVSLGDPNCKIDLSEFLIDG 300

QY 301 STIGKRRFRIOKOLLADVAQALDIPGAPLMGVQGDNDPHTFNLTHTNSRDLKTAI 360
D 301 STIGKRRFRIOKOLLADVAQALDIPGAPLMGVQGDNDPHTFNLTHTNSRDLKTAI 360
QY 361 EKITORGGLSNVGAISFVTNKFPSKANGNSGAPNVVVVVWDGMPDTDKVEASRLAES 420
D 361 EKITORGGLSNVGAISFVTNKFPSKANGNSGAPNVVVVVWDGMPDTDKVEASRLAES 420
QY 421 GINFFTTTIEGAANEQYVVEPNPANKAVCRITGPFSLHQSFWGLAKTLQPIVKKVCD 480
D 421 GINFFTTTIEGAANEQYVVEPNPANKAVCRITGPFSLHQSFWGLAKTLQPIVKKVCD 480
QY 481 TDRACKCTCLNSADIGFVIDGSSVGTGNFRVLOFPTNLTKFEISDTRIGAVOYT 540
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QY 541 YEORLFEGFDKSSKPDILNAIKKVGYSWGSGTSGAINFALQOLFKSKKPKKRLMTLI 600
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QY 601 TDGSSYDVRIPMAAHLKGVITTAIGVMAAOEELVIAHPARDHSFFVDEPDNLHOY 660
D 601 TDGSSYDVRIPMAAHLKGVITTAIGVMAAOEELVIAHPARDHSFFVDEPDNLHOY 660
QY 661 VPRIONICTEFSNQP RN 678
D 661 VPRIONICTEFSNQP RN 678

RESULT 11
US-09-989-293A-179
Sequence 179, Application US/09989293A
Patent No. 7034136
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/045787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1997-11-24

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PRIOR FILING DATE: 1998-02-25
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01

PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 678; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 VQSLSPRMRESFVLESKPKKGVTPSALTYSSSKSPAQAQETTKAYORPPIPGTTAQ 180
DB 121 VQSLSPRMRESFVLESKPKKGVTPSALTYSSSKSPAQAQETTKAYORPPIPGTTAQ 180
QY 181 PVTLMQILAVTVAVAPPTLPSPSPAASSTSI PRPOSCHROENDLWSTATYSSONR 240
DB 181 PVTLMQILAVTVAVAPPTLPSPSPAASSTSI PRPOSCHROENDLWSTATYSSONR 240
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DB 241 PRADPGIORODPSGAFAQKVGADVSLGLVPKEELSTOSLEPVSLDPPNCKIDLSPFLIDG 300
QY 301 STSIGRRFRIOQLIADVAQALDIGPAGPLMGVVOYGDNPATHEMLKHTNSRDLKTAI 360
DB 301 STSIGRRFRIOQLIADVAQALDIGPAGPLMGVVOYGDNPATHEMLKHTNSRDLKTAI 360
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DB 361 EKITORGASNVGRASIFVTKNFFSKANGRSGAPVVVVVVVGVGPTDKVEASRLARES 420
QY 421 GINIFFTIEGAENKQYVEEPFANKAVCRNCEYSLSHVQSMFGLHKTLOPLVRVCD 480
DB 421 GINIFFTIEGAENKQYVEEPFANKAVCRNCEYSLSHVQSMFGLHKTLOPLVRVCD 480
QY 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOPTNLTKEFEISDTDRIGAVQYT 540
DB 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOPTNLTKEFEISDTDRIGAVQYT 540
QY 541 YEORLFEPGPKYSKSDIINAIRVGVWGGTSTGAANPALEQLFKKSPNRRKIMILI 600
DB 541 YEORLFEPGPKYSKSDIINAIRVGVWGGTSTGAANPALEQLFKKSPNRRKIMILI 600
QY 601 TDRSYDDVRI PMAAHLKGVITYAIGVMAAOEELVIATHPARDHSFFVDFDMLHOY 660
DB 601 TDRSYDDVRI PMAAHLKGVITYAIGVMAAOEELVIATHPARDHSFFVDFDMLHOY 660
QY 661 VPRIIIONICTEFNSQPRN 678
DB 661 VPRIIIONICTEFNSQPRN 678

RESULT 12
US-09-394-264-5
; Sequence 5, Application US/09394264
; Patent No. 7030235
; GENERAL INFORMATION:
; APPLICANT: Morton, Cynthia C.
; APPLICANT: Robertson, Nahid G.

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; TITLE OF INVENTION: NOVEL COCHLEAR GENE COCH5B2 AND USES THEREOF
; FILE REFERENCE: 10286/008001
; CURRENT APPLICATION NUMBER: US/09/394,264
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: US 60/102,343
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-394-264-5

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      7 IDGSSSVG 14

RESULT 13
US-09-907-794A-227
; Sequence 227, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-227

Query Match      1.2%; Score 8; DB 2; Length 550;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      500 IDGSSSVG 507
Db      372 IDGSSSVG 379

RESULT 14
US-09-905-125A-227
; Sequence 227, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
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; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-905-125A-227
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Best Local Similarity 100.0%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      372 IDGSSSVG 379
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; Sequence 227, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jenie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 227
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-902-775A-227
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Best Local Similarity 100.0%; Pred. No. 58;
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Db      372 IDGSSSVG 379
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Job time : 53 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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(without alignments)
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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| 562 | 678 | 100.0 | 678 | 4 | US-10-174-587-150 Sequence 150, App |
| 626 | 678 | 100.0 | 678 | 4 | US-10-063-742-34 Sequence 34, App1 |
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| 752 | 678 | 100.0 | 678 | 6 | US-11-103-195-34 Sequence 34, App1 |
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| 755 | 328 | 48.4 | 329 | 4 | US-10-127-101-2 Sequence 2, App1 |
| 756 | 259 | 38.2 | 656 | 3 | US-09-801-736A-2 Sequence 2, App1 |
| 757 | 178 | 26.3 | 178 | 3 | US-09-801-736A-4 Sequence 4, App1 |
| 758 | 172 | 25.4 | 172 | 3 | US-09-864-761-47637 Sequence 47637, App |
| 759 | 171 | 25.2 | 171 | 3 | US-09-864-761-33310 Sequence 33310, App |
| 760 | 161 | 23.7 | 186 | 3 | US-09-764-870-301 Sequence 301, App |
| 761 | 161 | 23.7 | 186 | 3 | US-09-764-875-797 Sequence 797, App |
| 762 | 161 | 23.7 | 186 | 4 | US-10-125-540-301 Sequence 301, App |
| 763 | 84 | 12.4 | 160 | 4 | US-09-801-736A-3 Sequence 3, App1 |
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| 774 | 8 | 1.2 | 120 | 6 | US-11-096-568A-139 Sequence 139, App |
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| 778 | 8 | 1.2 | 124 | 6 | US-11-096-568A-140 Sequence 140, App |
| 779 | 8 | 1.2 | 133 | 4 | US-10-767-701-61822 Sequence 61822, App |
| 780 | 8 | 1.2 | 153 | 5 | US-10-739-930-9196 Sequence 9196, App |
| 781 | 8 | 1.2 | 159 | 3 | US-09-864-761-49020 Sequence 49020, App |
| 782 | 8 | 1.2 | 206 | 4 | US-10-425-115-278572 Sequence 278572, App |
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| 786 | 8 | 1.2 | 230 | 4 | US-10-282-122A-73662 Sequence 73662, App |
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| 790 | 8 | 1.2 | 248 | 4 | US-10-425-114-48915 Sequence 48915, App |
| 791 | 8 | 1.2 | 267 | 5 | US-10-732-923-5980 Sequence 5980, App |
| 792 | 8 | 1.2 | 341 | 6 | US-11-096-568A-20989 Sequence 20989, App |
| 793 | 8 | 1.2 | 349 | 4 | US-10-425-115-208114 Sequence 208114, App |
| 794 | 8 | 1.2 | 400 | 4 | US-10-282-122A-43293 Sequence 43293, App |
| 795 | 8 | 1.2 | 432 | 5 | US-10-357-819-32 Sequence 32, App1 |
| 796 | 8 | 1.2 | 452 | 6 | US-11-045-004-445 Sequence 445, App |
| 797 | 8 | 1.2 | 503 | 4 | US-10-108-260A-4457 Sequence 4457, App |
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| 1369 | 8 | 1.2 | 550 | 4 | US-10-289-937-227 Sequence 227, App |
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| 1389 | 8 | 1.2 | 550 | 4 | US-10-215-371-227 Sequence 227, App |
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| 1397 | 8 | 1.2 | 550 | 4 | US-10-771-187-227 Sequence 227, App |
| 1398 | 8 | 1.2 | 550 | 5 | US-10-963-467-227 Sequence 227, App |
| 1399 | 8 | 1.2 | 550 | 5 | US-10-978-255-227 Sequence 227, App |
| 1400 | 8 | 1.2 | 550 | 5 | US-10-970-823-227 Sequence 227, App |
| 1404 | 8 | 1.2 | 550 | 5 | US-10-156-761-10881 Sequence 10881, App |
| 1409 | 8 | 1.2 | 559 | 4 | US-11-097-143-44858 Sequence 24858, App |
| 1410 | 8 | 1.2 | 686 | 6 | US-10-359-493-18389 Sequence 18389, App |
| 1411 | 8 | 1.2 | 695 | 4 | US-10-424-599-183746 Sequence 183746, App |
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GenCore version 5.1.9
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 678 | 100.0 | 678 | US-10-196-749-150 | Sequence 150, App |
| 2 | 678 | 100.0 | 678 | US-11-101-316-34 | Sequence 34, App |
| 3 | 8 | 1.2 | 503 | US-11-293-697-497 | Sequence 4497, App |
| 4 | 8 | 1.2 | 550 | US-10-196-749-46 | Sequence 46, App |
| 5 | 7 | 1.0 | 91 | US-10-953-349-36732 | Sequence 36732, A |
| 6 | 7 | 1.0 | 99 | US-10-953-349-37027 | Sequence 37027, A |
| 7 | 7 | 1.0 | 126 | US-10-953-349-30530 | Sequence 30530, A |
| 8 | 7 | 1.0 | 128 | US-10-953-349-37026 | Sequence 37026, A |
| 9 | 7 | 1.0 | 142 | US-10-953-349-37025 | Sequence 37025, A |
| 10 | 7 | 1.0 | 170 | US-10-953-349-30529 | Sequence 30529, A |
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| 16 | 7 | 1.0 | 255 | US-10-953-349-20680 | Sequence 20680, A |
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| 23 | 7 | 1.0 | 310 | US-11-305-413-9 | Sequence 9, Appl |
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| 32 | 7 | 1.0 | 447 | US-10-953-349-26677 | Sequence 26677, A |
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| 39 | 7 | 1.0 | 557 | US-10-953-349-7230 | Sequence 7230, App |
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ALIGNMENTS

RESULT 1
US-10-196-749-150
Sequence 150, Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C340
CURRENT APPLICATION NUMBER: US/10/196, 749
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 150
LENGTH: 678
TYPE: PRT
ORGANISM: Homo Sapien
US-10-196-749-150

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-11-101-316-34
; Sequence 34, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P323ORIC17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; PRIOR FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06

;; PRIOR APPLICATION NUMBER: PCT/US00/23328
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: 09/380137
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; NUMBER OF SEQ ID NOS: 170
;; SEQ ID NO 34
;; LENGTH: 678
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-11-101-316-34

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Best Local Similarity 100.0%; Pred. No. 0;
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; Publication No. US20060105376A1
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; CURRENT FILING DATE: 2004-09-30
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; SOFTWARE: Patentin version 3.3
; SEQ ID NO 30530
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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 37026
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Query Match 1.0%; Score 7; DB 6; Length 128;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 20 LVTGVHS 26
DB 108 LVTGVHS 114
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RESULT 9

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US-10-953-349-37025
; Sequence 37025, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 37025
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37025
```

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Query Match 1.0%; Score 7; DB 6; Length 142;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 20 LVTGVHS 26
DB 111 LVTGVHS 114
```

```
DB 122 LVTGVHS 128
```

```
RESULT 10
US-10-953-349-30529
; Sequence 30529, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 30529
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-10-953-349-30529
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```
Query Match 1.0%; Score 7; DB 6; Length 170;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 251 DPGAAF 257
DB 73 DPGAAF 79
```

RESULT 11

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US-10-953-349-28247
; Sequence 28247, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 28247
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Trilicium aestivum
US-10-953-349-28247
```

```
Query Match 1.0%; Score 7; DB 6; Length 185;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 208 ASTTSIP 214
DB 92 ASTTSIP 98
```

```
RESULT 12
US-10-953-349-30528
; Sequence 30528, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 30528
```

LENGTH: 202
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-953-349-30528

Query Match
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 251 DPGGAF 257
Db 105 DPGGAF 111

RESULT 13
US-10-953-349-31820

Sequence 31820, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31820
LENGTH: 217
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-953-349-31820

Query Match
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 AVTVAVA 195
Db 155 AVTVAVA 161

RESULT 14
US-10-953-349-18707
Sequence 18707, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 18707
LENGTH: 246
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-18707

Query Match
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 SAASTTS 212
Db 127 SAASTTS 133

RESULT 15
US-10-953-349-31819
Sequence 31819, Application US/10953349

Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31819
LENGTH: 247
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-953-349-31819

Query Match
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 AVTVAVA 195
Db 185 AVTVAVA 191

Search completed: June 7, 2006, 01:59:31
Job time : 17 secs

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